

SCORE Search Results Details for Application
10687035 and Search Result
20070607_154734_us-10-687-035-
1_copy_14_452.rag.

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This page gives you Search Results detail for the Application 10687035 and Search Result 20070607_154734_us-10-687-035-1_copy_14_452.rag.

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OM protein - protein search, using sw model

Run on: June 7, 2007, 17:43:31 ; Search time 212 Seconds
(without alignments)

1013.289 Million cell updates/sec

Title: US-10-687-035-1_COPY_14_452

Perfect score: 2321

Sequence: 1 FTHRSSVSTTSTPTGPTVYL.....HGVTOLGEYVILDRDSLIFNG 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_200701:*

1: geneseqp1980s:*

2: geneseqp1950s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

10: geneseqp2006s:*

11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2321	100.0	748	8	ADS94302	AdS94302 CA 125/O7
2	2321	100.0	772	3	AAB12553	Abb12553 Human ova
3	2321	100.0	772	5	ABP30897	Abp30897 0772p clo
4	2321	100.0	772	7	ADA08541	Ada08541 Human ova
5	2321	100.0	772	7	ADF08884	Adf08884 Secreted
6	2321	100.0	772	7	ADG46171	Adg46171 Human ova
7	2321	100.0	772	9	ADX17767	Adx17767 Human ova
8	2321	100.0	809	8	ADS94303	AdS94303 CA 125/O7
9	2321	100.0	833	3	AAB12554	Abb12554 Human ova
10	2321	100.0	833	5	ABP30898	Abp30898 0772p clo
11	2321	100.0	833	7	ADA08542	Ada08542 Human ova
12	2321	100.0	833	7	ADF08885	Adf08885 Secreted
13	2321	100.0	833	7	ADG46172	Adg46172 Human ova
14	2321	100.0	833	9	ADX17768	Adx17768 Human ova
15	2321	100.0	914	3	AAB12552	Abb12552 Human ova
16	2321	100.0	914	4	AAB99203	Abb99203 Human ova
17	2321	100.0	914	5	ABP30968	Abp30968 Hypotheti
18	2321	100.0	914	5	ABP30896	Abp30896 0772p pro
19	2321	100.0	914	5	ADU01425	Adu01425 Breast ca
20	2321	100.0	914	5	ADZ41689	Adz41689 Human bre
21	2321	100.0	914	7	ADA08631	Ada08631 Human O77
22	2321	100.0	914	7	ADA08465	Ada08465 Human ova
23	2321	100.0	914	7	ADF08974	Adf08974 Secreted
24	2321	100.0	914	7	ADF08808	Adf08808 Secreted
25	2321	100.0	914	7	ADG46095	Adg46095 Human ova
26	2321	100.0	914	8	ADN40451	Adn40451 Human bre
27	2321	100.0	914	9	ADX17691	Adx17691 Human ova
28	2321	100.0	914	9	ADX17857	Adx17857 Partial h
29	2321	100.0	1485	8	ADP81174	Adp81174 Protein o
30	2317	99.8	748	10	AEK19871	Aek19871 CA 125 po
31	2317	99.8	1889	6	AAE34700	Aae34700 Protein e
32	2317	99.8	1890	5	ABG96381	Abg96381 Human ova
33	2317	99.8	1890	8	ADM12352	Adm12352 Human CA1
34	2317	99.8	1890	8	ADQ38574	Adq38574 Ovarian c
35	2317	99.8	1890	10	AEF01059	Aef01059 Ovarian c
36	2317	99.8	6995	9	AEC60057	Aec60057 Human muc
37	2317	99.8	6995	10	AEL74820	Ael74820 Cancer-as
38	2312	99.6	3451	5	ABP31026	Abp31026 Amino aci
39	2312	99.6	3451	7	ADA08748	Ada08748 Human O77
40	2312	99.6	3451	7	ADF09091	Adf09091 Secreted
41	2312	99.6	3451	9	ADX17974	Adx17974 Human ova
42	2301	99.1	1148	4	AAB95836	Abb95836 Human pro
43	2301	99.1	1148	5	ABB50283	Abb50283 HOST-1 ov
44	2301	99.1	1148	5	ABG96380	Abg96380 Human ova
45	2301	99.1	1148	5	ABP30964	Abp30964 Truncated

ALIGNMENTS

RESULT 1
ADS94302
ID ADS94302 standard; protein; 748 AA.

XX AD594302;
AC
XX
DT 02-DEC-2004 (first entry)
XX
DE CA 125/0772P 3-repeat amino acid sequence SEQ ID NO:1.
XX
KW antibody; antigen-binding antibody fragment;
KW cell-associated CA 125/0772P; monoclonal antibody; cytostatic;
KW immunostimulant; mediator of lysis; tumour; cell proliferative disorder;
KW cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;
KW ovarian cancer.
XX
OS Synthetic.
XX
XX WO2004035537-A2.
XX
XX 29-APR-2004.
XX
XX 15-OCT-2003; 2003WO-US032945.
XX
XX 16-OCT-2002; 2002US-0418828P.
XX
XX 10-JUL-2003; 2003US-0485986P.
XX
XX (EURO-) EUROCELTIQUE SA.
XX
XX Albane EF, Soltis DA;
XX
XX WPI: 2004-357171/33.
XX
XX
XX Novel isolated antibody, or antigen-binding antibody fragment binding
XX with cell-associated CA 125/0772P polypeptide relative to shed CA
XX 125/0772 polypeptide, useful for ameliorating cervical or ovarian cancer.
XX
XX Example; SEQ ID NO 1: 153pp; English.
XX
XX The present invention describes an isolated antibody, or an antigen-
XX binding antibody fragment (I), that preferentially binds cell-associated
XX CA 125/0772P polypeptide relative to shed CA 125/0772 polypeptide. Also
XX described: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2)
XX a monoclonal antibody that competes with binding of (II); (3) a hybridoma
XX as deposited in (II); (4) an isolated nucleic acid molecule (III)
XX comprising a nucleotide sequence that encodes a variable chain region of
XX (I); (5) a pharmaceutical composition comprising an antibody or an
XX antigen-binding antibody fragment that preferentially binds cell-
XX associated CA 125/0772P polypeptide relative to shed CA 125/0772P
XX polypeptide, and a carrier; (6) a pharmaceutical composition comprising a
XX monoclonal antibody or an antigen-binding monoclonal antibody fragment
XX that preferentially binds cell-associated CA 125/0772P polypeptide
XX relative to shed CA 125/0772P polypeptide, and a carrier; (7) an article
XX of manufacture (IV) comprising packaging material and a composition
XX comprising an antibody, or an antigen-binding antibody fragment that
XX preferentially binds cell-associated CA 125/0772P relative to shed CA
XX 125/0772P, and a carrier contained within the packaging material, and
XX composition in a form suitable for administration to a subject; (8) a
XX fusion polypeptide (V) comprising an antibody, or an antigen-binding
XX antibody fragment, which preferentially binds cell-associated CA
XX 125/0772P relative to shed CA 125/0772P operably linked to a heterologous
XX agent; (9) ameliorating (M1) a symptom of a CA 125/0772P-related disorder
XX i (10) a monoclonal antibody (VI) chosen from 325.1, 621.1, 633.1, 654.1,
XX 725.1, 869, 7F10, 8A1, 8AC3, 15C9, 8E3, 8B5, 7G10, 16C7, 7C6, 7H1, 16H9,

CC 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding
CC antibody fragment; (II) an antibody or antigen binding antibody fragment
CC that competes with (VI); and (12) a pharmaceutical composition comprising
CC (VI) and a carrier. (I) has cytostatic activity, and can be used as an
CC immunostimulant and a mediator of lysis of positive tumour cell. (I) is
CC useful for ameliorating a symptom of a CA 125/077P-related disorder which
CC is a cell proliferative disorder such as cancer, cervical or uterine
CC cancer, breast or lung cancer or ovarian cancer. (V) is useful
CC diagnostically for monitoring the development or progression of cancer or
CC tumour as part of clinical testing procedure. The present sequence
CC represents the CA 125/0772P 3-repeat amino acid sequence, which is used
CC in the exemplification of the present invention.
XX
SQ Sequence 748 AA;
Query Match 100.0%; Score 2321; DB 8; Length 748;
Best Local Similarity 100.0%; Pred. No. 3.4e-212;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTHRSSVSTTSPGPTVYLGASKTPASIFGPSAASHLLILFTLNTITNLRYEENWPG 60
Db 14 FTHRSSVSTTSPGPTVYLGASKTPASIFGPSAASHLLILFTLNTITNLRYEENWPG 73
QY 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPDPGTP 120
Db 74 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPDPGTP 133
QY 121 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 134 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
QY 181 INLRYNADWQPGSLKENITDNVMKLLSPLEFRSSLGARYTCRVIARLSVNGAETR 240
Db 194 INLRYNADWQPGSLKENITDNVMKLLSPLEFRSSLGARYTCRVIARLSVNGAETR 253
QY 241 VDLICTYLOPLSGCLPIKQVHELSQOHTGILRGVPSLDKDSLYLNGYNEPGDEPT 300
Db 254 VDLICTYLOPLSGCLPIKQVHELSQOHTGILRGVPSLDKDSLYLNGYNEPGDEPT 313
QY 301 TPKPATTFPLPULSEATTAMGYHLKTLTLNFTI SNLQYSPDMGKGSATFNSTEGVLQHLR 360
Db 314 TPKPATTFPLPULSEATTAMGYHLKTLTLNFTI SNLQYSPDMGKGSATFNSTEGVLQHLR 373
QY 361 PLFKSSMGPFYLGQQLISLRPEKOGAATGVDTCTYHPDPVPGGLDIOQLYWELSQLTH 420
Db 374 PLFKSSMGPFYLGQQLISLRPEKOGAATGVDTCTYHPDPVPGGLDIOQLYWELSQLTH 433
QY 421 GVTOLGFYVLDKDSLIFNG 439
Db 434 GVTOLGFYVLDKDSLIFNG 452
RESULT 2
AAB12553
ID AAB12553 standard; protein; 772 AA.
XX
AC AAB12553;
DT
XX 07-NOV-2000 (first entry)
XX
DE Human ovarian carcinoma antigen O772P protein SEQ ID NO:388.

XX Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KW tumour antigen; identification; cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX W02000036107-A2.
XX 22-JUN-2000.
XX 17-DEC-1999; 99WO-US030270.
XX 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, King GE, Algate PA, Frudakis TN;
XX WPI: 2000-431589/37.
DR N-PSDB; AAA70074.
XX
XX Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
PT encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer.
XX
XX Example 2; Page 197-200; 299pp; English.
XX
XX The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC cancer. AA69691 to AAA70077 and AAB12552 to AAB12557 represent human
CC ovarian carcinoma polynucleotides and proteins used in the
CC exemplification of the present invention
XX
XX Sequence 772 AA;

Query Match 100.0%; Score 2321; DB 3; Length 772;
Best Local Similarity 100.0%; Pred. No. 3.5e-212;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 FTHRSSVSTTSTGTPTVYLGASKTPASIFGPSAASHLLILFTLNTITNLRVEENWPG 60
Dy 159 FTHRSSVSTTSTGTPTVYLGASKTPASIFGPSAASHLLILFTLNTITNLRVEENWPG 218
Oy 61 SRKNTTERRVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGDAICTHRPDPTGP 120
Dy 219 SRKNTTERRVLOGLLRPLFKNTSVGLYSGCRLLTLRPEKDGATGDAICTHRPDPTGP 278
Oy 121 GLDRQLYLELSQTHSITELGTYTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNT 180
Dy 279 GLDRQLYLELSQTHSITELGTYTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNT 338
Oy 181 INNLRYMADMGQPGSLKFNITDNVKKHLLSPLFORSSLGARYTCGRVIALRSVKNGAETR 240
Dy 339 INNLRYMADMGQPGSLKFNITDNVKKHLLSPLFORSSLGARYTCGRVIALRSVKNGAETR 398

Oy 241 VDLCTYLIQPLSGPLPIKQVFHLSQQTHGITRLGYPYSLOKDSLYLNGYNEPGDEPPT 300
Dy 399 VDLCTYLIQPLSGPLPIKQVFHLSQQTHGITRLGYPYSLOKDSLYLNGYNEPGDEPPT 458
Oy 301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDKMGKSATFNSTGVLOHLR 360
Dy 459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDKMGKSATFNSTGVLOHLR 518
Oy 361 PLFQKSSMGPFYLGQCLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQQLYWEISQLTH 420
Dy 519 PLFQKSSMGPFYLGQCLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIQQLYWEISQLTH 578
Oy 421 GVTQLGFYVLDRLDSLFING 439
Dy 579 GVTQLGFYVLDRLDSLFING 597

RESULT 3
ABP30897
ID ABP30897 standard; protein; 772 AA.
XX
XX AC ABP30897;
XX
XX DT 02-JUL-2002 (first entry)
XX
XX DE 0772P clone 21013.
XX
XX KW Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.
XX
XX OS Homo sapiens.
XX
XX PN W0200206317-A2.
XX
XX PD 24-JAN-2002.
XX
XX PF 17-JUL-2001; 2001WO-US022635.
XX
XX PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
XX
XX (CORI-) CORIXA CORP.
XX
XX Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedwick TS, Carter D, Hill P, Albone E;
XX
XX WPI: 2002-164781/21.
DR N-PSDB; ABB72968.
XX
XX Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX
XX Example 2; Page 315-316; 408pp; English.
XX
XX This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion

CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents protein
CC related to the invention
XX
XX
SQ Sequence 772 AA;

Query Match 100.0%; Score 2321; DB 5; Length 772;
Best Local Similarity 100.0%; Pred. No. 3.5e-212;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDEATGVDAICTHRPDPGTP 120
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDEATGVDAICTHRPDPGTP 278
Qy 121 GLDREQLYLELSQTHSITELGPTTLDKDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITELGPTTLDKDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 181 INNLRYMADMGQPSLKFNITDNVMKHLSPFLFQSSILGARYTGCRRVIALRSVKNGAETR 240
Db 339 INNLRYMADMGQPSLKFNITDNVMKHLSPFLFQSSILGARYTGCRRVIALRSVKNGAETR 398
Qy 241 VOLLCITYLOPLSGPLPIKOVFHELSQOHTGTRIGPYSLDKDSLYLNGYNEPGDEPPT 300
Db 399 VOLLCITYLOPLSGPLPIKOVFHELSQOHTGTRIGPYSLDKDSLYLNGYNEPGDEPPT 458
Qy 301 TKPATTELPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
Db 459 TKPATTELPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 518
Qy 361 PLFQKSSMGFFYLGCQLISLRPEKOGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 420
Db 519 PLFQKSSMGFFYLGCQLISLRPEKOGAATGVDTTCTYHPDPVGPGLDIQQLYWELSQLTH 578
Qy 421 GVTQLGFEVLDKDSLFNG 439
Db 579 GVTQLGFEVLDKDSLFNG 597

RESULT 4
ADA08541
ID ADA08541 standard; protein; 772 AA.

AC ADA08541;
XX
XX 06-NOV-2003 (first entry)
XX Human ovarian carcinoma antigen O772P #1.
XX human; gene therapy; ovarian cancer; cancer.
XX Homo sapiens.
OS
XX
XX US2003091580-A1.
XX
XX
PD 15-MAY-2003.

XX 17-JUL-2001; 2001US-00907969.
PF
XX 18-JUN-2001; 2001US-00884441.
XX

PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.

XX Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedwick TS, Carter D, Hill P, Albone E;
XX
XX WPI; 2003-532352/50.

XX New isolated O772P polypeptides and polynucleotides, useful in gene
PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
PT cancer.

XX Example 2; SEQ ID NO 388; 371pp; English.

PS The invention relates to an isolated O772P polypeptide, which has the
XX structure fully defined in the specification. The composition containing
CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
CC or antigen presenting cells are useful for stimulating an immune response
CC and treating ovarian cancer. Detecting the presence of the
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
CC carcinoma cDNAs and protein cDNAs were identified using microarray
CC technology. The present sequence represents a human ovarian carcinoma
CC antigen.

XX SQ Sequence 772 AA;

Query Match 100.0%; Score 2321; DB 7; Length 772;
Best Local Similarity 100.0%; Pred. No. 3.5e-212;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDEATGVDAICTHRPDPGTP 120
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDEATGVDAICTHRPDPGTP 278
Qy 121 GLDREQLYLELSQTHSITELGPTTLDKDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITELGPTTLDKDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 181 INNLRYMADMGQPSLKFNITDNVMKHLSPFLFQSSILGARYTGCRRVIALRSVKNGAETR 240
Db 339 INNLRYMADMGQPSLKFNITDNVMKHLSPFLFQSSILGARYTGCRRVIALRSVKNGAETR 398
Qy 241 VOLLCITYLOPLSGPLPIKOVFHELSQOHTGTRIGPYSLDKDSLYLNGYNEPGDEPPT 300

Db 399 VDLCTYQLPSGGPIKQVHELSQOQTHGTRGLSPYSLDKDSLYLNGYNFPGDEPPT 458
QY 301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 360
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518
QY 361 PLFKSSMGPFYLGQQLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQOLYWELSQLTH 420
Db 519 PLFKSSMGPFYLGQQLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQOLYWELSQLTH 578
QY 421 GVTQLGFYVLDRLSLFNG 439
Db 579 GVTQLGFYVLDRLSLFNG 597

RESULT 5
ID ADF08884 standard; protein; 772 AA.
XX AC ADF08884;
XX DT 12-FEB-2004 (first entry)
XX DE Secreted ovarian carcinoma antigen seqid 388.
XX KW gene therapy; protein therapy; vaccine; antibody inhibition;
KW breast cancer; restorative therapy; diagnostic agent; immunoassay;
KW secreted ovarian carcinoma antigen.
XX OS Homo sapiens.
XX PN US2003124140-A1.
XX PD 03-JUL-2003.
XX PF 17-JUL-2002; 2002US-00198053.
XX PR 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
PR 17-JUL-2001; 2001US-00907969.
XX PA (CORI-) CORIXA CORP.
XX PI Bangur CS, Retter KW, Fanger GR, Hill P;
XX WPI: 2003-897152/82.
DR N-PSDB: ADF08881.
XX O: Oncogenic nucleic acids useful for the prevention, diagnosis and treatment of breast cancer.
XX PS Example 2; SEQ ID NO 388; 399pp; English.
XX

CC The invention describes nucleic acids (I) and the polypeptides (II) they encode. The nucleic acids (I) may be used for preventing, diagnosing and treating diseases related to their aberrant expression i.e. breast cancers. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (II) by expressing CC inactive proteins or to supplement the patients own production of (III). CC Additionally, (I) may be used to produce (II), by inserting (I) into a host cell and culturing the cell to express the protein (II). (I) And its CC complementary sequences may also be used as DNA probes in diagnostic CC assays to detect and quantitate the presence of similar nucleic acids in CC samples, and therefore which patients may be in need of restorative CC therapy. The host cell may also be used as antigens in the production of CC antibodies against (II) and in assays to identify modulators of (II)'s CC expression and activity. The anti-(II) antibodies, agonists and CC antagonists may be used to regulate expression and activity and as CC diagnostic agents for detecting the presence of (II) in samples (e.g. by CC immunoassay). This sequence represents a secreted ovarian carcinoma CC antigen.
XX XX
SQ Sequence 772 AA;
Query Match 100.0%; Score 2321; DB 7; Length 772;
Best Local Similarity 100.0%; Pred. No. 3.5e-212; Mismatches 0; Indels 0; Gaps 0;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNFTLNRYEENWPG 60
Db 159 FTHRSSVSTSTPGTPTVYLGASKTPASIFGSAASHLLILFTLNFTLNRYEENWPG 218
QY 61 SRKFTTTERVLOGLLRPLFKNTSVGPLYSGCRUTLLRPEKDGATGVAICTHRPDPTGP 120
Db 219 SRKFTTTERVLOGLLRPLFKNTSVGPLYSGCRUTLLRPEKDGATGVAICTHRPDPTGP 278
QY 121 GLDREQLYLELSQLTHSITELGPLYTLDRDSLXVNGFTHRSSVPTTSTGVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQLTHSITELGPLYTLDRDSLXVNGFTHRSSVPTTSTGVSEEPFTLNFT 338
QY 181 INNLRYMADMGQPGSLKFNITDNVVKHLLSPFORSSILGARYTCRVIALRSVKNGAETR 240
Db 339 INNLRYMADMGQPGSLKFNITDNVVKHLLSPFORSSILGARYTCRVIALRSVKNGAETR 398
QY 241 VDLCTYQLPSGGPIKQVHELSQOQTHGTRGLSPYSLDKDSLYLNGYNFPGDEPPT 300
Db 399 VDLCTYQLPSGGPIKQVHELSQOQTHGTRGLSPYSLDKDSLYLNGYNFPGDEPPT 458
QY 301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 360
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLR 518
QY 361 PLFKSSMGPFYLGQQLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQOLYWELSQLTH 420
Db 519 PLFKSSMGPFYLGQQLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQOLYWELSQLTH 578
QY 421 GVTQLGFYVLDRLSLFNG 439
Db 579 GVTQLGFYVLDRLSLFNG 597

RESULT 6
ADG46171

ID	ADG46171 standard; protein; 772 AA.
XX	
AC	ADG46171;
XX	
DT	26-FEB-2004 (first entry)
XX	
DE	Human ovarian carcinoma polypeptide #2.
XX	
KW	Human; ovarian carcinoma; O8E; ovarian cancer; secreted tumour antigen;
KW	cytostatic; 0772P.
XX	
OS	Homo sapiens.
XX	
PN	US2003165504-A1.
XX	
PD	04-SEP-2003.
XX	
PF	04-APR-2001; 2001US-00827271.
XX	
PR	17-DEC-1998; 98US-00215681.
PR	17-DEC-1998; 98US-00216003.
PR	23-JUN-1999; 99US-00338933.
PR	24-SEP-1999; 99US-00404879.
PR	17-JUL-2000; 2000US-00617747.
PR	10-AUG-2000; 2000US-00636801.
PR	20-SEP-2000; 2000US-00667857.
XX	
PA	(RETT/) RETTER M W.
PA	(FANG/) FANGER G R.
XX	
PI	Retter MW, Fanger GR;
XX	
DR	WPI; 2003-898035/82.
XX	
PT	New isolated O8E or 0772P polypeptides, useful for diagnosing,
PT	preventing, treating and monitoring cancer, e.g. ovarian cancer,
XX	stimulating the immune response in patient.
XX	
PS	Claim 5; SEQ ID NO 388; 290pp; English.
XX	
CC	The invention relates to human ovarian carcinoma polypeptides, designated
CC	O8E or 0772P, and the polynucleotides encoding them. The invention also
CC	relates to methods for inhibiting the development of cancer, e.g. ovarian
CC	cancer in a patient, methods for stimulating and/or expanding T cells and
CC	methods for identifying secreted tumour antigens. The polypeptides,
CC	compositions, antibodies to the polypeptides and methods are useful for
CC	diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
CC	cancer. The composition is particularly useful for stimulating an immune
CC	response in patient. This sequence represents a human ovarian carcinoma
CC	polypeptide of the invention.
XX	
SQ	Sequence 772 AA:
	Query Match 100.0%; Score 2321; DB 7; Length 772;
	Best Local Similarity 100.0%; Pred. No. 3.5e-212;
	Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWMPG 60
DB	159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLFTITNLRYEENWMPG 218

QY	61 SRKFNTERVIOGLLRPLFKNTSVGPLYSGCRLTLRLAPEKDGATGVDAICTHRPDPPTGP 120
DB	219 SRKFNTERVIOGLLRPLFKNTSVGPLYSGCRLTLRLAPEKDGATGVDAICTHRPDPPTGP 278
QY	121 GLDREQLYLELSQLTHTSITELGPYTLDRDLSLVNGFTHRSSVPTTSTGVSSEEPFTLNFT 180
DB	279 GLDREQLYLELSQLTHTSITELGPYTLDRDLSLVNGFTHRSSVPTTSTGVSSEEPFTLNFT 338
QY	181 INNLRYMADMGQPSGLKFNITDNWKHLSPILFQRSSILGARYTGCRVIALRSVKNGAETR 240
DB	339 INNLRYMADMGQPSGLKFNITDNWKHLSPILFQRSSILGARYTGCRVIALRSVKNGAETR 398
QY	241 VDLLCTYLQPLSGPGLPIKOVFHELSSOOTHGITRLGPIYSLDKDSLYLNGYNRPDPDEPT 300
DB	399 VDLLCTYLQPLSGPGLPIKOVFHELSSOOTHGITRLGPIYSLDKDSLYLNGYNRPDPDEPT 458
QY	301 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATNSTEGVIOHLRL 360
DB	459 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATNSTEGVIOHLRL 518
QY	361 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYWELSQLTH 420
DB	519 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVGPGLDIOQLYWELSQLTH 578
QY	421 GVTQLGFYVLDROSLFING 439
DB	579 GVTQLGFYVLDROSLFING 597
RESULT 7	
ADX17767	
ID	ADX17767 standard; protein; 772 AA.
XX	
AC	ADX17767;
XX	
DT	21-APR-2005 (first entry)
XX	
DE	Human ovarian carcinoma antigen cDNA 0772P clone 21013 encoded protein.
XX	
KW	diagnosis; cytostatic; immunostimulant; gene therapy; tumor;
KW	ovarian tumor; cancer; carcinoma; antigen.
XX	
OS	Homo sapiens.
XX	
PN	US2005031634-A1.
XX	
PD	10-FEB-2005.
XX	
PF	02-JUN-2004; 2004US-00860790.
XX	
PR	17-DEC-1998; 98US-00216003.
PR	23-JUN-1999; 99US-00338933.
PR	24-SEP-1999; 99US-00404879.
PR	17-JUL-2000; 2000US-00617747.
PR	10-AUG-2000; 2000US-00636801.
PR	20-SEP-2000; 2000US-00667857.
PR	04-APR-2001; 2001US-00827271.
PR	18-JUN-2001; 2001US-00884441.
PR	17-JUL-2001; 2001US-00907969.
PR	17-JUL-2002; 2002US-00198053.
XX	

PA (CORI-) CORIXA CORP.
XX Bangur CS, Retter KW, Fanger GR, Hill P;
XX WPI: 2005-151645/16.
XX
XX New ovarian carcinoma polynucleotides, preferably cDNAs, useful for
PT diagnosing, preventing and treating diseases, such as ovarian cancer, and
PT for eliciting humoral and/or cellular immune response.
XX
XX Example 2: SEQ ID NO 388; 398pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising a sequence
CC of, a sequence hybridizing under highly stringent conditions to, or
CC having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in
CC the specification, its complement or degenerate variants, or a sequence
CC of at least 20 contiguous residues of the 849 or 1399 bp sequence. The
CC polynucleotides and polypeptides are useful for diagnosing, preventing
CC and treating diseases, such as ovarian cancer, and for eliciting humoral
CC and/or cellular immune response. This sequence corresponds to an ovarian
CC carcinoma antigen protein of the invention.
XX
XX Sequence 772 AA;

Query Match 100.0%; Score 2321; DB 9; Length 772;
Best Local Similarity 100.0%; Pred. No. 3.5e-212;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIEGSPAASHLLILFTLNFTINLRYEENMWPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIEGSPAASHLLILFTLNFTINLRYEENMWPG 218
Qy 61 SKKNTTERRVLOGLLRPLFNKTSVGPYSGCRTLLRPEKDGATGVAICTHRPDPGTP 120
Db 219 SKKNTTERRVLOGLLRPLFNKTSVGPYSGCRTLLRPEKDGATGVAICTHRPDPGTP 278
Qy 121 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVFTTSTGWSSEPFPLNFT 180
Db 279 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVFTTSTGWSSEPFPLNFT 338
Qy 181 INNLRYADMGQPGSLKFNITDNVKKHLLSPLFORSSLGARYTCGRVIALRSVKNCAETR 240
Db 339 INNLRYADMGQPGSLKFNITDNVKKHLLSPLFORSSLGARYTCGRVIALRSVKNCAETR 398
Qy 241 VDLICTTYLQPLSGPLPIKOVFHELSSQOHTGTRGLPGYSLDKDSLYLNGYNKPGDEPPT 300
Db 399 VDLICTTYLQPLSGPLPIKOVFHELSSQOHTGTRGLPGYSLDKDSLYLNGYNKPGDEPPT 458
Qy 301 TPKPATTPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKGSATNSTEGVLQHLR 360
Db 459 TPKPATTPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKGSATNSTEGVLQHLR 518
Qy 361 PLFPQKSSMGPFYLGQQLISLRPEKOGAATGVTTCCTYHPDPVCGPLDIOQLYWELSQLTH 420
Db 519 PLFPQKSSMGPFYLGQQLISLRPEKOGAATGVTTCCTYHPDPVCGPLDIOQLYWELSQLTH 578
Qy 421 GVTQLGYFVLDRDSLIFNG 439
Db 579 GVTQLGYFVLDRDSLIFNG 597

RESULT 8
ADS94303
ID ADS94303 standard; protein; 809 AA.
XX
XX
AC ADS94303;
XX
XX 02-DEC-2004 (first entry)
XX
XX CA 125/0772P 3-repeat TM amino acid sequence SEQ ID NO:2.
XX
XX antibody; antigen-binding antibody fragment;
KW cell-associated CA 125/0772P; monoclonal antibody; cytostatic;
KW immunostimulant; mediator of lysis; tumour; cell proliferative disorder;
KW cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;
KW ovarian cancer.
XX
XX Synthetic.
XX
XX WO2004035537-A2.
XX
XX 29-APR-2004.
XX
XX 15-OCT-2003; 2003WO-US032945.
XX
XX 16-OCT-2002; 2002US-0418828P.
PR 10-JUL-2003; 2003US-0485986P.
XX
XX (EURO-) EUROCELTIQUE SA.
XX
XX Albone EF, Soltis DA;
XX WPI: 2004-357171/33.
XX
XX Novel isolated antibody, or antigen-binding antibody fragment binding
PT with cell-associated CA 125/0772P polypeptide relative to shed CA
PT 125/0772 polypeptide, useful for ameliorating cervical or ovarian cancer.
XX
XX Example; SEQ ID NO 2; 153pp; English.
XX
XX The present invention describes an isolated antibody, or an antigen-
CC binding antibody fragment (I), that preferentially binds cell-associated
CC CA 125/0772P polypeptide relative to shed CA 125/0772 polypeptide. Also
CC described: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2)
CC a monoclonal antibody that competes with binding of (II); (3) a hybridoma
CC as deposited in (II); (4) an isolated nucleic acid molecule (III)
CC comprising a nucleotide sequence that encodes a variable chain region of
CC (II); (5) a pharmaceutical composition comprising an antibody or an
CC antigen-binding antibody fragment that preferentially binds cell-
CC associated CA 125/0772P polypeptide relative to shed CA 125/0772P
CC polypeptide, and a carrier; (6) a pharmaceutical composition comprising a
CC monoclonal antibody or an antigen-binding monoclonal antibody fragment
CC that preferentially binds cell-associated CA 125/0772P polypeptide
CC relative to shed CA 125/0772P polypeptide, and a carrier; (7) an article
CC of manufacture (IV) comprising packaging material and a composition
CC comprising an antibody, or an antigen-binding antibody fragment that
CC preferentially binds cell-associated CA 125/0772P relative to shed CA
CC 125/0772P, and a carrier contained within the packaging material, and
CC composition in a form suitable for administration to a subject; (8) a
CC fusion polypeptide (V) comprising an antibody, or an antigen-binding
CC antibody fragment, which preferentially binds cell-associated CA
CC 125/0772P relative to shed CA 125/0772P operably linked to a heterologous

CC agent; (9) ameliorating (M1) a symptom of a CA 125/O772P-related disorder
CC ; (10) a monoclonal antibody (VI) chosen from 325.1, 621.1, 633.1, 654.1,
CC 725.1, 869, 7F10, 8A1, 8AC3, 15C9, 8E3, 8B5, 7G10, 16C7, 7C6, 7H1, 16H9,
CC 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding
CC antibody fragment; (11) an antibody or antigen binding antibody fragment
CC that competes with (VI); and (12) a pharmaceutical composition comprising
CC (VI) and a carrier. (I) has cytostatic activity, and can be used as an
CC immunostimulant and a mediator of lysis of positive tumour cell. (I) is
CC useful for ameliorating a symptom of a CA 125/O77P-related disorder which
CC is a cell proliferative disorder such as cancer, cervical or uterine
CC cancer, breast or lung cancer or ovarian cancer. (VI) is useful
CC diagnostically for monitoring the development or progression of cancer or
CC tumour as part of clinical testing procedure. The present sequence
CC represents the CA 125/O772P 3-repeat TM amino acid sequence, which is
CC used in the exemplification of the present invention.
XX
SQ Sequence 809 AA;

Query Match 100.0%; Score 2321; DB 8; Length 809;
Best Local Similarity 100.0%; Pred. No. 3.8e-212;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTPTGPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 60
Db 14 FTHRSSVSTTPTGPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 73
Qy 61 SRKENTTERVLOGLLRPLFKNTSGPLYSGCRLLTLRLPEKDGATGVDAICTHRPDPTGP 120
Db 74 SRKENTTERVLOGLLRPLFKNTSGPLYSGCRLLTLRLPEKDGATGVDAICTHRPDPTGP 133
Qy 121 GLDREQLYLELSQTHSITELGPTYLDROSLYVNGFTHRSSVPTTSTGVSSEEPFTLNFT 180
Db 134 GLDREQLYLELSQTHSITELGPTYLDROSLYVNGFTHRSSVPTTSTGVSSEEPFTLNFT 193
Qy 181 INNLRYMADMOPGSLKFNITDNVMKHLLSPILFORSSIGARYTGCRVIALRSYKNGAETR 240
Db 194 INNLRYMADMOPGSLKFNITDNVMKHLLSPILFORSSIGARYTGCRVIALRSYKNGAETR 253
Qy 241 VDLICTYIQPLSGPLPIKQVFHELSQOOTHGITRLGYSIDKDSLYLNGYNEFGPDEPPT 300
Db 254 VDLICTYIQPLSGPLPIKQVFHELSQOOTHGITRLGYSIDKDSLYLNGYNEFGPDEPPT 313
Qy 301 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
Db 314 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 373
Qy 361 PLFOKSSMGPFYLCQILSLRPEKDGAAVTCTYHPDPVGPGLDIOQLYWELSQLTH 420
Db 374 PLFOKSSMGPFYLCQILSLRPEKDGAAVTCTYHPDPVGPGLDIOQLYWELSQLTH 433
Qy 421 GVTQLGFYVLDROSLFNG 439
Db 434 GVTQLGFYVLDROSLFNG 452

RESULT 9
ID AAB12554
XX AAB12554 standard; protein: 833 AA.
AC AAB12554;
XX

DT 07-NOV-2000 (first entry)
XX Human ovarian carcinoma antigen O772P protein SEQ ID NO:389.
DE
XX Human: ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KW tumour antigen; identification; cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX WO200036107-A2.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99WO-US030270.
XX
PR 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
XX
PA (CORI-) CORIXA CORP.

PI Mitcham JL, King GE, Algate PA, Frudakis TN;
XX
DR WPI; 2000-431589/37.
DR N-PSDB; AAA70075.
XX
PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
PT encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer.
XX
PS Example 2; Page 200-203; 299pp; English.
XX
CC The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human
CC ovarian carcinoma polynucleotides and proteins used in the
CC exemplification of the present invention
XX
SQ Sequence 833 AA;

Query Match 100.0%; Score 2321; DB 3; Length 833;
Best Local Similarity 100.0%; Pred. No. 4e-212;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FTHRSSVSTTPTGPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 60
Db 78 FTHRSSVSTTPTGPTVYLGASKTPASIFGSAASHLLILFTLNFTITNLRYEENWPG 137
Qy 61 SRKENTTERVLOGLLRPLFKNTSGPLYSGCRLLTLRLPEKDGATGVDAICTHRPDPTGP 120
Db 138 SRKENTTERVLOGLLRPLFKNTSGPLYSGCRLLTLRLPEKDGATGVDAICTHRPDPTGP 197
Qy 121 GLDREQLYLELSQTHSITELGPTYLDROSLYVNGFTHRSSVPTTSTGVSSEEPFTLNFT 180
Db 198 GLDREQLYLELSQTHSITELGPTYLDROSLYVNGFTHRSSVPTTSTGVSSEEPFTLNFT 257

Qy	181	INNLRYMADMGQPSGLKFNITDNVVKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR	240
Db	258	INNLRYMADMGQPSGLKFNITDNVVKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR	317
Qy	241	VDLLCTYLGPSGGLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT	300
Db	318	VDLLCTYLGPSGGLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT	377
Qy	301	TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLQHLR	360
Db	378	TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLQHLR	437
Qy	361	PLFQKSSMGPFYLGCOLISLRPEKDGAATGVDTTCTYHPDPVPGGLDIQQLYWELSQUTH	420
Db	438	PLFQKSSMGPFYLGCOLISLRPEKDGAATGVDTTCTYHPDPVPGGLDIQQLYWELSQUTH	497
Qy	421	GVTQLGEYVLDKDSLFING	439
Db	498	GVTQLGEYVLDKDSLFING	516
RESULT 10			
ABP30898			
ID	ABP30898 standard; protein: 833 AA.		
AC	ABP30898;		
XX			
DT	02-JUL-2002 (first entry)		
XX			
DE	0772P clone 21003.		
XX			
KW	Human; immunostimulant; cytostatic; cancer; ovarian carcinoma.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200206317-A2.		
XX			
PD	24-JAN-2002.		
XX			
PF	17-JUL-2001; 2001WO-US022635.		
XX			
PR	17-JUL-2000; 2000US-00617747.		
PR	10-AUG-2000; 2000US-00636801.		
PR	20-SEP-2000; 2000US-00667857.		
PR	04-APR-2001; 2001US-00827271.		
PR	18-JUN-2001; 2001US-00884441.		
XX			
PA	(CORI-) CORIXA CORP.		
XX			
PI	Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;		
PI	Reed SG, Vedvick TS, Carter D, Hill P, Albone E;		
XX			
XX	WPI; 2002-164781/21.		
DR	N-PSDB; ABN72969.		
DR			
XX			
PT	Polypeptides comprising an immunogenic portion of an ovarian carcinoma		
PT	protein or its variants, useful for stimulating an immune response in a		
PT	patient and treating ovarian cancer.		
XX			
PS	Example 2; Page 316-318; 408pp; English.		
XX			

CC	This invention relates to polypeptides comprising an immunogenic portion			
CC	of an ovarian carcinoma protein which acts as an immunostimulant and is			
CC	cytostatic. The polypeptides, polynucleotides, antibodies, fusion			
CC	proteins, T cell populations and antigen presenting cells that express			
CC	the polypeptides are useful for stimulating an immune response in a			
CC	patient and treating ovarian cancer. This sequence represents protein			
CC	related to the invention			
XX				
Qy	Sequence 833 AA;			
Query Match 100.0%; Score 2321; DB 5; Length 833;				
Best Local Similarity 100.0%; Pred. No. 4e-212;				
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1	FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG	60	
Db	78	FTHRSSVSTTSTPGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG	137	
Qy	61	SRKFNMTTERVLOGLLRPLFKNTSVGPLYSGCRLTLRPEKDGEATGDAICTHRPDPPTG	120	
Db	138	SRKFNMTTERVLOGLLRPLFKNTSVGPLYSGCRLTLRPEKDGEATGDAICTHRPDPPTG	197	
Qy	121	GLDREQLYLELSQUTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT	180	
Db	198	GLDREQLYLELSQUTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT	257	
Qy	181	INNLRYMADMGQPSGLKFNITDNVVKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR	240	
Db	258	INNLRYMADMGQPSGLKFNITDNVVKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR	317	
Qy	241	VDLLCTYLGPSGGLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT	300	
Db	318	VDLLCTYLGPSGGLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT	377	
Qy	301	TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR	360	
Db	378	TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR	437	
Qy	361	PLFQKSSMGPFYLGCOLISLRPEKDGAATGVDTTCTYHPDPVPGGLDIQQLYWELSQUTH	420	
Db	438	PLFQKSSMGPFYLGCOLISLRPEKDGAATGVDTTCTYHPDPVPGGLDIQQLYWELSQUTH	497	
Qy	421	GVTQLGEYVLDKDSLFING	439	
Db	498	GVTQLGEYVLDKDSLFING	516	
RESULT 11				
ADA08542				
ID	ADA08542 standard; protein: 833 AA.			
XX				
AC	ADA08542;			
XX				
DT	06-NOV-2003 (first entry)			
XX				
DE	Human ovarian carcinoma antigen O772P #2.			
XX				
KW	human; gene therapy; ovarian cancer; cancer.			
XX				
OS	Homo sapiens.			
XX				

PN	US2003091580-A1.	
XX		
PD	15-MAY-2003.	
XX		
PF	17-JUL-2001; 2001US-00907969.	
XX		
PR	18-JUN-2001; 2001US-00884441.	
XX		
PA	(MITC/) MITCHAM J L.	
PA	(KING/) KING G E.	
PA	(ALGA/) ALGATE P A.	
PA	(FLIN/) FLING S P.	
PA	(RETT/) RETTER M W.	
PA	(FANG/) FANGER G R.	
PA	(REED/) REED S G.	
PA	(VEDV/) VEDVICK T S.	
PA	(CART/) CARTER D.	
PA	(HILL/) HILL P.	
PA	(ALBO/) ALBONE E.	
XX		
PI	Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;	
PI	Reed SG, Vedvick TS, Carter D, Hill P, Albone E;	
XX		
DR	WPI; 2003-532352/50.	
XX		
PT	New isolated 0772P polypeptides and polynucleotides, useful in gene	
PT	therapy, particularly for treating or diagnosing cancer, e.g. ovarian	
PT	cancer.	
XX		
PS	Example 2; SEQ ID NO 389; 37lpp; English.	
XX		
CC	The invention relates to an isolated 0772P polypeptide, which has the	
CC	structure fully defined in the specification. The composition containing	
CC	the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells	
CC	or antigen presenting cells are useful for stimulating an immune response	
CC	and treating ovarian cancer. Detecting the presence of the	
CC	polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian	
CC	carcinoma cDNAs and protein cDNAs were identified using microarray	
CC	technology. The present sequence represents a human ovarian carcinoma	
CC	antigen.	
XX		
SQ	Sequence 833 AA;	
Query Match 100.0%; Score 2321; DB 7; Length 833;		
Best Local Similarity 100.0%; Pred. No. 4e-212;		
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 FTHRSSVTTTPTGTTVYLGASKTPASIFGPSAASHLLILFTLNFITNLRYEENMWPG 60	
DB	78 FTHRSSVTTTPTGTTVYLGASKTPASIFGPSAASHLLILFTLNFITNLRYEENMWPG 137	
QY	61 SRKFTTERTVLOGLLRPLEKNTSVGLYSGCRLTLRLRPEKGEATGVDAICTHRPDPTGP 120	
DB	138 SRKFTTERTVLOGLLRPLEKNTSVGLYSGCRLTLRLRPEKGEATGVDAICTHRPDPTGP 197	
QY	121 GLDREQLYLELSQTHSITELGFTYLDROSLYVNGFTHRSSVPTTSTGWSVEEPTFLNFT 180	
DB	198 GLDREQLYLELSQTHSITELGFTYLDROSLYVNGFTHRSSVPTTSTGWSVEEPTFLNFT 257	
QY	181 INNLRYADMGQPSLKFNTDNVWKHLLSPLFQRSSISLGARYTGCRVIALRSVKNGAETR 240	

DB	258 INNLRYADMGQPSLKFNTDNVWKHLLSPLFQRSSISLGARYTGCRVIALRSVKNGAETR 317	
QY	241 VDLCTYLOPLSGPLPIKQVFEHLSQOQTHGTRIGLPYSLDKOSLYLNGYNEPGDPPEPT 300	
DB	318 VDLCTYLOPLSGPLPIKQVFEHLSQOQTHGTRIGLPYSLDKOSLYLNGYNEPGDPPEPT 377	
QY	301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKSGSATFNSTEGVLQHLR 360	
DB	378 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKSGSATFNSTEGVLQHLR 437	
QY	361 PLFKKSSMGPFYLGCOLISLRPEKDGATGVTCTYHPDPVPGGLDIQOLYNELSQLTH 420	
DB	438 PLFKKSSMGPFYLGCOLISLRPEKDGATGVTCTYHPDPVPGGLDIQOLYNELSQLTH 497	
QY	421 GVTOLGFYVLDROSLIFNG 439	
DB	498 GVTOLGFYVLDROSLIFNG 516	
RESULT 12		
ADF08885		
ID	ADF08885 standard; protein; 833 AA.	
XX		
AC	ADF08885;	
XX		
DT	12-FEB-2004 (first entry)	
XX		
DE	Secreted ovarian carcinoma antigen seqid 389.	
XX		
KW	gene therapy; protein therapy; vaccine; antibody inhibition;	
KW	breast cancer; restorative therapy; diagnostic agent; immunoassay;	
KW	secreted ovarian carcinoma antigen.	
OS	Homo sapiens.	
XX		
PN	US2003124140-A1.	
XX		
PD	03-JUL-2003.	
XX		
PF	17-JUL-2002; 2002US-00198053.	
XX		
PR	17-DEC-1998; 98US-00215681.	
PR	17-DEC-1998; 98US-00216003.	
PR	23-JUN-1999; 99US-00338933.	
PR	24-SEP-1999; 99US-00404879.	
PR	17-JUL-2000; 2000US-00617747.	
PR	10-AUG-2000; 2000US-00636801.	
PR	20-SEP-2000; 2000US-00667857.	
PR	04-APR-2001; 2001US-00827271.	
PR	18-JUN-2001; 2001US-00884441.	
PR	17-JUL-2001; 2001US-00907969.	
XX		
PA	(CORI-) CORIXA CORP.	
XX		
PI	Bangur CS, Retter MW, Fanger GR, Hill P;	
XX		
DR	WPI; 2003-897152/82.	
DR	N-PSDB; ADF08882.	
XX		
PT	Oncogenic nucleic acids useful for the prevention, diagnosis and	
PT	treatment of breast cancer.	

XX PS Example 2; SEQ ID NO 389; 399pp; English.

XX The invention describes nucleic acids (I) and the polypeptides (II) they

CC encode. The nucleic acids (I) may be used for preventing, diagnosing and

CC treating diseases related to their aberrant expression i.e. breast

CC cancers. For example, (I) and (II) may be used to treat disorders

CC associated with decreased expression by rectifying mutations or deletions

CC in a patient's genome that affect the activity of (II) by expressing

CC inactive proteins or to supplement the patients own production of (II).

CC Additionally, (I) may be used to produce (II), by inserting (I) into a

CC host cell and culturing the cell to express the protein (II). (I) And its

CC complementary sequences may also be used as DNA probes in diagnostic

CC assays to detect and quantitate the presence of similar nucleic acids in

CC samples, and therefore which patients may be in need of restorative

CC therapy. The host cell may also be used as antigens in the production of

CC antibodies against (II) and in assays to identify modulators of (II)'s

CC expression and activity. The anti-(II) antibodies, agonists and

CC antagonists may be used to regulate expression and activity and as

CC diagnostic agents for detecting the presence of (II) in samples (e.g. by

CC immunoassay). This sequence represents a secreted ovarian carcinoma

CC antigen.

XX SQ Sequence 833 AA;

Query Match 100.0%; Score 2321; DB 7; Length 833;

Best Local Similarity 100.0%; Pred. No. 4e-212;

Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTGTCTPVYLGASKTPASIFGSPSAASHLLILFTLNTITNLRYEENWPG 60

DB 78 FTHRSSVSTTGTCTPVYLGASKTPASIFGSPSAASHLLILFTLNTITNLRYEENWPG 137

QY 61 SRKFNTERVLOGLLRPLFKNTSGVLYSGCRLTLRPEKDEATGVDAICTHRDPDTPG 120

DB 138 SRKFNTERVLOGLLRPLFKNTSGVLYSGCRLTLRPEKDEATGVDAICTHRDPDTPG 197

QY 121 GLDREQLYELSLQTHSITELGPYTLDRSLYVNGFTHRSSVPTTSTGVVSEEPFTLNET 180

DB 198 GLDREQLYELSLQTHSITELGPYTLDRSLYVNGFTHRSSVPTTSTGVVSEEPFTLNET 257

QY 181 INNLRYADMCGQSGSLKFNITDNVMKHLSPFORSSLGARYTCGRVIALRSVKNGAETR 240

DB 258 INNLRYADMCGQSGSLKFNITDNVMKHLSPFORSSLGARYTCGRVIALRSVKNGAETR 317

QY 241 VDLICTYLOPLSGPLPIKQVFHELSQOQTHGTRLGPYSIDKDSLXLYNGYNEFGPDEPPT 300

DB 318 VDLICTYLOPLSGPLPIKQVFHELSQOQTHGTRLGPYSIDKDSLXLYNGYNEFGPDEPPT 377

QY 301 TPKPATTELPPLSEATFANGVHLKTLTLNFTISNLQVSPDMGKGSATFNSTGVLOHLR 360

DB 378 TPKPATTELPPLSEATFANGVHLKTLTLNFTISNLQVSPDMGKGSATFNSTGVLOHLR 437

QY 361 PLFOKSSMGPFYLCOLISLRAPEKGAATGVDTCTYVHPDPVPGCLDIQOOLYWELSLQTH 420

DB 438 PLFOKSSMGPFYLCOLISLRAPEKGAATGVDTCTYVHPDPVPGCLDIQOOLYWELSLQTH 497

QY 421 GVTQLGFYVLDRLDSLFING 439

DB 498 GVTQLGFYVLDRLDSLFING 516

RESULT 13

ADG46172

ID ADG46172 standard; protein; 833 AA.

XX

AC ADG46172;

XX

DT 26-FEB-2004 (first entry)

XX

DE Human ovarian carcinoma polypeptide #3.

XX

KW Human; ovarian carcinoma; O8E; ovarian cancer; secreted tumour antigen;

KW cytostatic; O772P.

XX

OS Homo sapiens.

XX

PN US2003165504-A1.

XX

PD 04-SEP-2003.

XX

PF 04-APR-2001; 2001US-00827271.

XX

PR 17-DEC-1998; 98US-00215681.

PR 17-DEC-1998; 98US-00216003.

PR 23-JUN-1999; 99US-00338933.

PR 24-SEP-1999; 99US-00404879.

PR 17-JUL-2000; 2000US-00617747.

PR 10-AUG-2000; 2000US-00636801.

PR 20-SEP-2000; 2000US-00667857.

XX

PA (RETT/) RETTER M W.

PA (FANG/) FANGER G R.

XX

PI Retter MW, Fanger GR;

XX

DR WPI; 2003-898035/82.

XX

PT New isolated O8E or O772P polypeptides, useful for diagnosing,

PT preventing, treating and monitoring cancer, e.g. ovarian cancer,

PT stimulating the immune response in patient.

XX

PS Claim 5; SEQ ID NO 389; 290pp; English.

XX

CC The invention relates to human ovarian carcinoma polypeptides, designated

CC O8E or O772P, and the polynucleotides encoding them. The invention also

CC relates to methods for inhibiting the development of cancer, e.g. ovarian

CC cancer in a patient, methods for stimulating and/or expanding T cells and

CC methods for identifying secreted tumour antigens. The polypeptides, for

CC compositions, antibodies to the polypeptides and methods are useful for

CC diagnosing, preventing, treating and monitoring cancer, e.g. ovarian

CC cancer. The composition is particularly useful for stimulating an immune

CC response in patient. This sequence represents a human ovarian carcinoma

CC polypeptide of the invention.

XX

SQ Sequence 833 AA;

Query Match 100.0%; Score 2321; DB 7; Length 833;

Best Local Similarity 100.0%; Pred. No. 4e-212;

Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTGTCTPVYLGASKTPASIFGSPSAASHLLILFTLNTITNLRYEENWPG 60

Db	78	FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG	137
Qy	61	SRKENTTERRVLOGLLRPLFKNTSGPLYSGCRLTLRLPEKDGATGDAICTHRPDPGTP	120
Db	138	SRKENTTERRVLOGLLRPLFKNTSGPLYSGCRLTLRLPEKDGATGDAICTHRPDPGTP	197
Qy	121	GLDREQLYLELSQLSHITELGPTTLDRDSLYVNGFTHRSSVPTTSTGWSVEEPTFLNFT	180
Db	198	GLDREQLYLELSQLSHITELGPTTLDRDSLYVNGFTHRSSVPTTSTGWSVEEPTFLNFT	257
Qy	181	INNLRYMADMGQPSGLKENITDNVKKHLLSPLFQRSSLGARYTGCRRVIALRSVKNGAETR	240
Db	258	INNLRYMADMGQPSGLKENITDNVKKHLLSPLFQRSSLGARYTGCRRVIALRSVKNGAETR	317
Qy	241	VDLLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEFGPDEPPT	300
Db	318	VDLLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEFGPDEPPT	377
Qy	301	TPKPATTFELPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR	360
Db	378	TPKPATTFELPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR	437
Qy	361	PLFKSSMGPFYLGCOLISLRPEKDGAAATGVTCTYHPDPVGPGLDIQOLYWELSOLTH	420
Db	438	PLFKSSMGPFYLGCOLISLRPEKDGAAATGVTCTYHPDPVGPGLDIQOLYWELSOLTH	497
Qy	421	GVTQLGFEYVLDNRDSLIFNG	439
Db	498	GVTQLGFEYVLDNRDSLIFNG	516
Qy	421	GVTQLGFEYVLDNRDSLIFNG	439
Db	498	GVTQLGFEYVLDNRDSLIFNG	516
RESULT 14			
ADX17768			
ID	ADX17768	standard; protein; 833 AA.	
XX			
AC	ADX17768;		
XX			
DT	21-APR-2005	(first entry)	
XX			
DE	Human ovarian carcinoma antigen cDNA 0772P clone 21003 encoded protein.		
XX			
KW	diagnosis; cytostatic; immunostimulant; gene therapy; tumor;		
XX	ovarian tumor; cancer; carcinoma; antigen.		
OS	Homo sapiens.		
XX			
PN	US2005031634-A1.		
XX			
PD	10-FEB-2005.		
XX			
PF	02-JUN-2004; 2004US-00860790.		
XX			
PR	17-DEC-1998; 98US-00216003.		
PR	23-JUN-1999; 99US-00338933.		
PR	24-SEP-1999; 99US-00404879.		
PR	17-JUL-2000; 2000US-00617747.		
PR	10-AUG-2000; 2000US-00636801.		
PR	20-SEP-2000; 2000US-00667857.		
PR	04-APR-2001; 2001US-00827271.		
PR	18-JUN-2001; 2001US-00884441.		

PR	17-JUL-2001; 2001US-00907969.		
PR	17-JUL-2002; 2002US-00198053.		
XX			
PA	(CORI-) CORIXA CORP.		
XX			
PI	Bangur CS, Retter MW, Fanger GR, Hill P;		
XX			
XX	WPI; 2005-151645/16.		
XX	New ovarian carcinoma polynucleotides, preferably cDNAs, useful for		
PT	diagnosing, preventing and treating diseases, such as ovarian cancer, and		
PT	for eliciting humoral and/or cellular immune response.		
XX			
PS	Example 2; SEQ ID NO 389; 398pp; English.		
XX			
CC	The invention relates to an isolated polynucleotide comprising a sequence		
CC	of, a sequence hybridizing under highly stringent conditions to, or		
CC	having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in		
CC	the specification, its complement or degenerate variants, or a sequence		
CC	of at least 20 contiguous residues of the 849 or 1399 bp sequence. The		
CC	polynucleotides and polypeptides are useful for diagnosing, preventing		
CC	and treating diseases, such as ovarian cancer, and for eliciting humoral		
CC	and/or cellular immune response. This sequence corresponds to an ovarian		
CC	carcinoma antigen protein of the invention.		
XX			
SQ	Sequence 833 AA;		
	Query Match 100.0%; Score 2321; DB 9; Length 833;		
	Best Local Similarity 100.0%; Pred. No. 4e-212;		
	Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1	FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG	60
Db	78	FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG	137
Qy	61	SRKENTTERRVLOGLLRPLFKNTSGPLYSGCRLTLRLPEKDGATGDAICTHRPDPGTP	120
Db	138	SRKENTTERRVLOGLLRPLFKNTSGPLYSGCRLTLRLPEKDGATGDAICTHRPDPGTP	197
Qy	121	GLDREQLYLELSQLSHITELGPTTLDRDSLYVNGFTHRSSVPTTSTGWSVEEPTFLNFT	180
Db	198	GLDREQLYLELSQLSHITELGPTTLDRDSLYVNGFTHRSSVPTTSTGWSVEEPTFLNFT	257
Qy	181	INNLRYMADMGQPSGLKENITDNVKKHLLSPLFQRSSLGARYTGCRRVIALRSVKNGAETR	240
Db	258	INNLRYMADMGQPSGLKENITDNVKKHLLSPLFQRSSLGARYTGCRRVIALRSVKNGAETR	317
Qy	241	VDLLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEFGPDEPPT	300
Db	318	VDLLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEFGPDEPPT	377
Qy	301	TPKPATTFELPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR	360
Db	378	TPKPATTFELPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR	437
Qy	361	PLFKSSMGPFYLGCOLISLRPEKDGAAATGVTCTYHPDPVGPGLDIQOLYWELSOLTH	420
Db	438	PLFKSSMGPFYLGCOLISLRPEKDGAAATGVTCTYHPDPVGPGLDIQOLYWELSOLTH	497
Qy	421	GVTQLGFEYVLDNRDSLIFNG	439

Db 498 GVTQLGFYVLDRLDSLFING 516

RESULT 15
AAB12552
ID AAB12552 standard; protein; 914 AA.
XX AC AAB12552;
XX 07-NOV-2000 (first entry)
DT Human ovarian carcinoma antigen O772P protein SEQ ID NO:312.
XX
KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
KW tumour antigen; identification; cytostatic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
PN W0200036107-A2.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99WO-US030270.
XX
PR 17-DEC-1998; 98US-00215681.
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Frudakis TN;
XX
DR WPI: 2000-431589/37.
DR N-PSDB; AAA70001.
XX
PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
PT encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer.
XX
PS Example 2; Page 172-174; 299pp; English.
XX
CC The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human
CC ovarian carcinoma polynucleotides and proteins used in the
CC exemplification of the present invention
XX
SQ Sequence 914 AA;

Query Match 100.0%; Score 2321; DB 3; Length 914;
Best Local Similarity 100.0%; Pred. No. 4,6e-212;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTSGTPTVYLKASTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60
|||||
DB 159 FTHRSSVSTTSGTPTVYLKASTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218

QY 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSCRLTLRLPEKDGATGVDAICTHRPDPGTP 120
|||||
DB 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSCRLTLRLPEKDGATGVDAICTHRPDPGTP 278
|||||
QY 121 GLDREQLYLELSQLTHSITELGPTVTLDRDSLXVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
|||||
DB 279 GLDREQLYLELSQLTHSITELGPTVTLDRDSLXVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
|||||
QY 181 INNLRYMADWQPGSLKFNITDNVWKHLSPLFQSSLGARYTGCRRVIALRSVKNGAETR 240
|||||
DB 339 INNLRYMADWQPGSLKFNITDNVWKHLSPLFQSSLGARYTGCRRVIALRSVKNGAETR 398
|||||
QY 241 VDLICTYLOPLSGFGLPIKQVFHELSSQOHTGTRLGYPYSLDKDSLXLNGYNEPGDEPPT 300
|||||
DB 399 VDLICTYLOPLSGFGLPIKQVFHELSSQOHTGTRLGYPYSLDKDSLXLNGYNEPGDEPPT 458
|||||
QY 301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATENSTEGVLOHLR 360
|||||
DB 459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATENSTEGVLOHLR 518
|||||
QY 361 PLFOKSSMGPFYLGQQLISLRPEKDGAAATGVDTCTYHPDPVPGGLDIQQLYWELSQLTH 420
|||||
DB 519 PLFOKSSMGPFYLGQQLISLRPEKDGAAATGVDTCTYHPDPVPGGLDIQQLYWELSQLTH 578
|||||
QY 421 GVTQLGFYVLDRLDSLFING 439
|||||
DB 579 GVTQLGFYVLDRLDSLFING 597

Search completed: June 7, 2007, 17:52:44
Job time : 215 secs

SCORE 2.0 BuildDate: 12/05/2005

**SCORE Search Results Details for Application
10687035 and Search Result
20070607_154741_us-10-687-035-
1_copy_14_452.rai.**

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OM protein - protein search, using sw model

Run on: June 7, 2007, 17:51:47 ; Search time 115 Seconds
(without alignments)
334.139 Million cell updates/sec

Title: US-10-687-035-1_COPY_14_452

Perfect score: 2321
Sequence: 1 FTRHSVSTTSTGTPTVYL.....HGVTLGFYVLDROSLFNG 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
- 1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep.*
 - 2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep.*
 - 3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep.*
 - 4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep.*
 - 5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PTUS_COMB.pep.*
 - 6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep.*
 - 7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2321	100.0	772	2	US-09-404-879A-388	Sequence 388, App
2	2321	100.0	772	2	US-09-667-857-388	Sequence 388, App
3	2321	100.0	772	2	US-10-198-053-388	Sequence 388, App
4	2321	100.0	772	2	US-09-827-271-388	Sequence 388, App
5	2321	100.0	833	2	US-09-404-879A-389	Sequence 389, App
6	2321	100.0	833	2	US-09-667-857-389	Sequence 389, App
7	2321	100.0	833	2	US-10-198-053-389	Sequence 389, App
8	2321	100.0	833	2	US-09-827-271-389	Sequence 389, App
9	2321	100.0	914	2	US-09-404-879A-312	Sequence 312, App
10	2321	100.0	914	2	US-09-338-933-312	Sequence 312, App
11	2321	100.0	914	2	US-09-667-857-312	Sequence 312, App
12	2321	100.0	914	2	US-10-198-053-312	Sequence 312, App
13	2321	100.0	914	2	US-10-198-053-478	Sequence 478, App
14	2321	100.0	914	2	US-09-827-271-312	Sequence 312, App
15	2312	99.6	3451	2	US-10-198-053-595	Sequence 595, App
16	2301	99.1	1148	2	US-10-198-053-458	Sequence 458, App
17	2301	99.1	1148	2	US-10-198-053-479	Sequence 479, App
18	2301	99.1	1148	2	US-09-827-271-458	Sequence 458, App
19	2301	99.1	1156	2	US-10-198-053-459	Sequence 459, App
20	2301	99.1	1156	2	US-09-827-271-459	Sequence 459, App
21	1436	61.9	304	2	US-10-198-053-486	Sequence 486, App
22	842.5	36.3	294	2	US-10-198-053-487	Sequence 487, App
23	814	35.1	313	2	US-10-198-053-461	Sequence 461, App
24	814	35.1	313	2	US-09-827-271-461	Sequence 461, App
25	809	34.9	155	2	US-10-198-053-591	Sequence 591, App
26	800	34.5	150	2	US-10-198-053-593	Sequence 593, App
27	697	30.0	134	2	US-10-198-053-592	Sequence 592, App
28	675.5	28.1	210	2	US-10-198-053-481	Sequence 481, App
29	662	28.5	230	2	US-10-198-053-480	Sequence 480, App
30	659.5	28.4	156	2	US-10-198-053-589	Sequence 589, App
31	651.5	28.1	156	2	US-10-198-053-596	Sequence 596, App
32	648	27.9	438	2	US-09-404-879A-390	Sequence 390, App
33	648	27.9	438	2	US-09-667-857-390	Sequence 390, App
34	648	27.9	438	2	US-10-198-053-390	Sequence 390, App
35	648	27.9	438	2	US-10-198-053-483	Sequence 483, App
36	648	27.9	438	2	US-09-827-271-390	Sequence 390, App
37	637.5	27.5	156	2	US-10-198-053-590	Sequence 590, App
38	611.5	26.3	268	2	US-10-198-053-485	Sequence 485, App
39	607.5	26.2	156	2	US-10-198-053-584	Sequence 584, App
40	600.5	25.9	156	2	US-10-198-053-587	Sequence 587, App
41	599.5	25.8	156	2	US-10-198-053-583	Sequence 583, App
42	598.5	25.8	156	2	US-10-198-053-586	Sequence 586, App
43	595.5	25.7	156	2	US-10-198-053-588	Sequence 588, App
44	592.5	25.5	156	2	US-10-198-053-580	Sequence 580, App
45	589.5	25.4	156	2	US-10-198-053-577	Sequence 577, App

ALIGNMENTS

RESULT 1
US-09-404-879A-388
; Sequence 388, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.

; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-879A-388

Query Match 100.0%; Score 2321; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTGTCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
Db 159 FTHRSSVSTTGTCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGEATGVDAICTHRPDPTGP 120
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGEATGVDAICTHRPDPTGP 278
Qy 121 GLDREQLYLELSQTHSITEIGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITEIGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 181 INNLRYMADMQGQSGSLKFNITDNVMKHLSPFORSSLGARTGCRVIALRSVKNKAETR 240
Db 339 INNLRYMADMQGQSGSLKFNITDNVMKHLSPFORSSLGARTGCRVIALRSVKNKAETR 398
Qy 241 VDLCTYLOPLSGGPIKQVHFELSQOOTHGITRLGYPYSLDKDSLYLNGYNERGPDPEPT 300
Db 399 VDLCTYLOPLSGGPIKQVHFELSQOOTHGITRLGYPYSLDKDSLYLNGYNERGPDPEPT 458
Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLYQSPDMGKGSATFNSTEGVLOHLR 360
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLYQSPDMGKGSATFNSTEGVLOHLR 518
Qy 361 PLFKSSKGPYILGCQLISLRPEKOGAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
Db 519 PLFKSSKGPYILGCQLISLRPEKOGAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 578
Qy 421 GVTQLGFVLDROSLFING 439
Db 579 GVTQLGFVLDROSLFING 597

RESULT 2
US-09-667-857-388
; Sequence 388, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462CS
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-667-857-388

Query Match 100.0%; Score 2321; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTGTCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
Db 159 FTHRSSVSTTGTCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGEATGVDAICTHRPDPTGP 120
Db 219 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGEATGVDAICTHRPDPTGP 278
Qy 121 GLDREQLYLELSQTHSITEIGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITEIGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 181 INNLRYMADMQGQSGSLKFNITDNVMKHLSPFORSSLGARTGCRVIALRSVKNKAETR 240
Db 339 INNLRYMADMQGQSGSLKFNITDNVMKHLSPFORSSLGARTGCRVIALRSVKNKAETR 398
Qy 241 VDLCTYLOPLSGGPIKQVHFELSQOOTHGITRLGYPYSLDKDSLYLNGYNERGPDPEPT 300
Db 399 VDLCTYLOPLSGGPIKQVHFELSQOOTHGITRLGYPYSLDKDSLYLNGYNERGPDPEPT 458
Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLYQSPDMGKGSATFNSTEGVLOHLR 360
Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLYQSPDMGKGSATFNSTEGVLOHLR 518
Qy 361 PLFKSSKGPYILGCQLISLRPEKOGAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
Db 519 PLFKSSKGPYILGCQLISLRPEKOGAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 578
Qy 421 GVTQLGFVLDROSLFING 439
Db 579 GVTQLGFVLDROSLFING 597

RESULT 3
US-10-198-053-388
; Sequence 388, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.

```
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-388

Query Match      100.0%; Score 2321; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218

Qy 61 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRUTLLRPEKDGATGVDAICTHRPDPTGP 120
Db 219 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRUTLLRPEKDGATGVDAICTHRPDPTGP 278

Qy 121 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVSEEPFTLNFT 338

Qy 181 INNLRYWADMGQPGSLKFNITDNVWKHLLSPLFORSSLGARYTCRCVIALRSVKNGAETR 240
Db 339 INNLRYWADMGQPGSLKFNITDNVWKHLLSPLFORSSLGARYTCRCVIALRSVKNGAETR 398

Qy 241 VDLICTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLINGYNEPGDEPPT 300
Db 399 VDLICTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLINGYNEPGDEPPT 458

Qy 301 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKSATNSTEGVLOHLLR 360
Db 459 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKSATNSTEGVLOHLLR 518

Qy 361 PLFQKSSMGPFYLGCOLISURPEKDGAAATGVDTCTYHPDPVPGGLDIOQLYWELSQLTH 420
Db 519 PLFQKSSMGPFYLGCOLISURPEKDGAAATGVDTCTYHPDPVPGGLDIOQLYWELSQLTH 578

Qy 421 GVTQLGFGYVLDROSLFNG 439
Db 579 GVTQLGFGYVLDROSLFNG 597

RESULT 4
US-09-827-271-388
; Sequence 388, Application US/09827271
; Patent No. 6962980
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
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; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-388

Query Match      100.0%; Score 2321; DB 2; Length 772;
Best Local Similarity 100.0%; Pred. No. 1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218

Qy 61 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRUTLLRPEKDGATGVDAICTHRPDPTGP 120
Db 219 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRUTLLRPEKDGATGVDAICTHRPDPTGP 278

Qy 121 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVSEEPFTLNFT 338

Qy 181 INNLRYWADMGQPGSLKFNITDNVWKHLLSPLFORSSLGARYTCRCVIALRSVKNGAETR 240
Db 339 INNLRYWADMGQPGSLKFNITDNVWKHLLSPLFORSSLGARYTCRCVIALRSVKNGAETR 398

Qy 241 VDLICTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLINGYNEPGDEPPT 300
Db 399 VDLICTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLINGYNEPGDEPPT 458

Qy 301 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKSATNSTEGVLOHLLR 360
Db 459 TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKSATNSTEGVLOHLLR 518

Qy 361 PLFQKSSMGPFYLGCOLISURPEKDGAAATGVDTCTYHPDPVPGGLDIOQLYWELSQLTH 420
Db 519 PLFQKSSMGPFYLGCOLISURPEKDGAAATGVDTCTYHPDPVPGGLDIOQLYWELSQLTH 578

Qy 421 GVTQLGFGYVLDROSLFNG 439
Db 579 GVTQLGFGYVLDROSLFNG 597

RESULT 5
US-09-404-879A-389
; Sequence 389, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
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; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-404-879A-389

Query Match      100.0%; Score 2321; DB 2; Length 833;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAAASHLLILFTLNFTITNLRYEENWMPG 60
    |||||||
Db 78 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAAASHLLILFTLNFTITNLRYEENWMPG 137

Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 120
    |||||||
Db 138 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 197

Qy 121 GLDREQYLLELSQTHSITELGPTYLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||||||
Db 198 GLDREQYLLELSQTHSITELGPTYLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257

Qy 181 INNLRYADMGPQSLKFNITDNVKKHLLSPLFORSSLGARYTGCRRVIALRSVKNGAETR 240
    |||||||
Db 258 INNLRYADMGPQSLKFNITDNVKKHLLSPLFORSSLGARYTGCRRVIALRSVKNGAETR 317

Qy 241 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 300
    |||||||
Db 318 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 377

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLOHLLR 360
    |||||||
Db 378 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLOHLLR 437

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIOQLYWELSQLTH 420
    |||||||
Db 438 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIOQLYWELSQLTH 497

Qy 421 GVTOLGFYVLDSDSLFING 439
    |||||||
Db 498 GVTOLGFYVLDSDSLFING 516

RESULT 6
US-09-667-857-389
; Sequence 389, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
```

```
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-667-857-389

Query Match      100.0%; Score 2321; DB 2; Length 833;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAAASHLLILFTLNFTITNLRYEENWMPG 60
    |||||||
Db 78 FTHRSSVSTSTPGTPTVYLGASKTPASIFGPSAAASHLLILFTLNFTITNLRYEENWMPG 137

Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 120
    |||||||
Db 138 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 197

Qy 121 GLDREQYLLELSQTHSITELGPTYLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||||||
Db 198 GLDREQYLLELSQTHSITELGPTYLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257

Qy 181 INNLRYADMGPQSLKFNITDNVKKHLLSPLFORSSLGARYTGCRRVIALRSVKNGAETR 240
    |||||||
Db 258 INNLRYADMGPQSLKFNITDNVKKHLLSPLFORSSLGARYTGCRRVIALRSVKNGAETR 317

Qy 241 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 300
    |||||||
Db 318 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 377

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLOHLLR 360
    |||||||
Db 378 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATNSTEGVLOHLLR 437

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIOQLYWELSQLTH 420
    |||||||
Db 438 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIOQLYWELSQLTH 497

Qy 421 GVTOLGFYVLDSDSLFING 439
    |||||||
Db 498 GVTOLGFYVLDSDSLFING 516

RESULT 7
US-10-198-053-389
; Sequence 389, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
```

; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-389

Query Match 100.0%; Score 2321; DB 2; Length 833;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTPGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
|||||
Db 78 FTHRSSVSTSTPGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 137

Qy 61 SRKFNTERVIOGLLRPLFKNTSVGPLYSGCRLLLRPEKDGATGDAICTHRPDTGP 120
|||||
Db 138 SRKFNTERVIOGLLRPLFKNTSVGPLYSGCRLLLRPEKDGATGDAICTHRPDTGP 197

Qy 121 GLDREQLYLELSOLTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 180
|||||
Db 198 GLDREQLYLELSOLTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 257

Qy 181 INNLRYMADMGQPSLKFNITDNVWKHLLSPLFORSSIGARYTGCRRVIALRSVKNGAETR 240
|||||
Db 258 INNLRYMADMGQPSLKFNITDNVWKHLLSPLFORSSIGARYTGCRRVIALRSVKNGAETR 317

Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPLYSLDKDSLYLYNGYNEPGDEPPT 300
|||||
Db 318 VDLCTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPLYSLDKDSLYLYNGYNEPGDEPPT 377

Qy 301 TPKPATTFLLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMGKGSATNSTEGVLOHLLR 360
|||||
Db 378 TPKPATTFLLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMGKGSATNSTEGVLOHLLR 437

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
|||||
Db 438 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 497

Qy 421 GVTQLGFEYVLDRLDSLIFNG 439
|||||
Db 498 GVTQLGFEYVLDRLDSLIFNG 516

RESULT 8
US-09-827-271-389
; Sequence 389, Application US/09827271
; Patent No. 6962980
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 389

; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-389

Query Match 100.0%; Score 2321; DB 2; Length 833;
Best Local Similarity 100.0%; Pred. No. 1.1e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTPGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
|||||
Db 78 FTHRSSVSTSTPGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 137

Qy 61 SRKFNTERVIOGLLRPLFKNTSVGPLYSGCRLLLRPEKDGATGDAICTHRPDTGP 120
|||||
Db 138 SRKFNTERVIOGLLRPLFKNTSVGPLYSGCRLLLRPEKDGATGDAICTHRPDTGP 197

Qy 121 GLDREQLYLELSOLTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 180
|||||
Db 198 GLDREQLYLELSOLTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 257

Qy 181 INNLRYMADMGQPSLKFNITDNVWKHLLSPLFORSSIGARYTGCRRVIALRSVKNGAETR 240
|||||
Db 258 INNLRYMADMGQPSLKFNITDNVWKHLLSPLFORSSIGARYTGCRRVIALRSVKNGAETR 317

Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPLYSLDKDSLYLYNGYNEPGDEPPT 300
|||||
Db 318 VDLCTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPLYSLDKDSLYLYNGYNEPGDEPPT 377

Qy 301 TPKPATTFLLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMGKGSATNSTEGVLOHLLR 360
|||||
Db 378 TPKPATTFLLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMGKGSATNSTEGVLOHLLR 437

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
|||||
Db 438 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 497

Qy 421 GVTQLGFEYVLDRLDSLIFNG 439
|||||
Db 498 GVTQLGFEYVLDRLDSLIFNG 516

RESULT 9
US-09-404-879A-312
; Sequence 312, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 312
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien

US-09-404-879A-312

Query Match 100.0%; Score 2321; DB 2; Length 914;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218

Qy 61 SRKENTTERRVLOGLLRPLFKNTSVGLYSGCRJTLRLPEKDEATGVDAICTHRPDPGTP 120
Db 219 SRKENTTERRVLOGLLRPLFKNTSVGLYSGCRJTLRLPEKDEATGVDAICTHRPDPGTP 278

Qy 121 GLDRQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 279 GLDRQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

Qy 181 INNLRYMADMGQPGSLKNTITDNVMKHLSPFORSSLGARYTCRVIALRSVKNGAETR 240
Db 339 INNLRYMADMGQPGSLKNTITDNVMKHLSPFORSSLGARYTCRVIALRSVKNGAETR 398

Qy 241 VOLLCTYLOPLSGPGLPIKOVFHELSSQTHGITRLGYPYSLDKDSLXLYNGYNEPGDEPPT 300
Db 399 VOLLCTYLOPLSGPGLPIKOVFHELSSQTHGITRLGYPYSLDKDSLXLYNGYNEPGDEPPT 458

Qy 301 TPKPATTLPPLSEATTANGYHLKTLTNFTISNLQYSPDMKGSATFNSTEGVLQHLRL 360
Db 459 TPKPATTLPPLSEATTANGYHLKTLTNFTISNLQYSPDMKGSATFNSTEGVLQHLRL 518

Qy 361 PLFOKSSNGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQOLYWELSOLTH 420
Db 519 PLFOKSSNGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQOLYWELSOLTH 578

Qy 421 GVTOLGFYVLDROSLFING 439
Db 579 GVTOLGFYVLDROSLFING 597

RESULT 10

US-09-338-933-312

; Sequence 312, Application US/09338933

; Patent No. 648931

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer Lynn

; APPLICANT: King, Gordon E.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF

; TITLE OF INVENTION: OVARIAN CANCER

; FILE REFERENCE: 210121.462C1

; CURRENT APPLICATION NUMBER: US/09/338,933

; CURRENT FILING DATE: 1999-06-23

; NUMBER OF SEQ ID NOS: 312

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 312

; LENGTH: 914

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-338-933-312

Query Match 100.0%; Score 2321; DB 2; Length 914;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;

Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218

Qy 61 SRKENTTERRVLOGLLRPLFKNTSVGLYSGCRJTLRLPEKDEATGVDAICTHRPDPGTP 120
Db 219 SRKENTTERRVLOGLLRPLFKNTSVGLYSGCRJTLRLPEKDEATGVDAICTHRPDPGTP 278

Qy 121 GLDRQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 279 GLDRQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

Qy 181 INNLRYMADMGQPGSLKNTITDNVMKHLSPFORSSLGARYTCRVIALRSVKNGAETR 240
Db 339 INNLRYMADMGQPGSLKNTITDNVMKHLSPFORSSLGARYTCRVIALRSVKNGAETR 398

Qy 241 VOLLCTYLOPLSGPGLPIKOVFHELSSQTHGITRLGYPYSLDKDSLXLYNGYNEPGDEPPT 300
Db 399 VOLLCTYLOPLSGPGLPIKOVFHELSSQTHGITRLGYPYSLDKDSLXLYNGYNEPGDEPPT 458

Qy 301 TPKPATTLPPLSEATTANGYHLKTLTNFTISNLQYSPDMKGSATFNSTEGVLQHLRL 360
Db 459 TPKPATTLPPLSEATTANGYHLKTLTNFTISNLQYSPDMKGSATFNSTEGVLQHLRL 518

Qy 361 PLFOKSSNGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQOLYWELSOLTH 420
Db 519 PLFOKSSNGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIQOLYWELSOLTH 578

Qy 421 GVTOLGFYVLDROSLFING 439
Db 579 GVTOLGFYVLDROSLFING 597

RESULT 11

US-09-667-857-312

; Sequence 312, Application US/09667857

; Patent No. 669964

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer L.

; APPLICANT: King, Gordon E.

; APPLICANT: Algate, Paul A.

; APPLICANT: Fling, Steven P.

; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary Richard

; APPLICANT: Reed, Steven G.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

; FILE REFERENCE: 210121.462C5

; CURRENT APPLICATION NUMBER: US/09/667,857

; CURRENT FILING DATE: 2000-09-20

; NUMBER OF SEQ ID NOS: 455

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 312

; LENGTH: 914

; TYPE: PRT

; ORGANISM: Homo sapien

US-09-667-857-312

Query Match									
Best Local Similarity 100.0%; Score 2321; DB 2; Length 914;									
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	FTHRSSVSTTSGTPTTVILGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG	60						
Db	159	FTHRSSVSTTSGTPTTVILGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG	218						
Qy	61	SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGDAICTHRDPDPTGP	120						
Db	219	SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGDAICTHRDPDPTGP	278						
Qy	121	GLDREQLYLELSOLTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT	180						
Db	279	GLDREQLYLELSOLTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT	338						
Qy	181	INNLRYMADMGQPSGLKFNITDNVWKHLSPLEFQSSSLGARYTGCRRVIALRSVKNGAETR	240						
Db	339	INNLRYMADMGQPSGLKFNITDNVWKHLSPLEFQSSSLGARYTGCRRVIALRSVKNGAETR	398						
Qy	241	VOLLCTVLOPLSGPLPIKOVFHELSSQOHTGITRLGPYSLDKDSLJNGYNEPGDEPPT	300						
Db	399	VOLLCTVLOPLSGPLPIKOVFHELSSQOHTGITRLGPYSLDKDSLJNGYNEPGDEPPT	458						
Qy	301	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKSATFNSTEGVLOHLRL	360						
Db	459	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKSATFNSTEGVLOHLRL	518						
Qy	361	PLFQKSSMGPFYLGCOLISLRPEKOGAATGVTCTTCTYHPDPVPGGLDIOQLYWELSQLTH	420						
Db	519	PLFQKSSMGPFYLGCOLISLRPEKOGAATGVTCTTCTYHPDPVPGGLDIOQLYWELSQLTH	578						
Qy	421	GVTQLGFVYLDRLDSLFG	439						
Db	579	GVTQLGFVYLDRLDSLFG	597						
RESULT 12									
US-10-198-053-312									
; Sequence 312 Application US/10198053									
; Patent No. 6858710									
; GENERAL INFORMATION:									
; APPLICANT: Bangur, Chaitanya S.									
; APPLICANT: Retter, Marc W.									
; APPLICANT: Fanger, Gary R.									
; APPLICANT: Hill, Paul									
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY									
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER									
; FILE REFERENCE: 210121.462C9									
; CURRENT APPLICATION NUMBER: US/10/198,053									
; CURRENT FILING DATE: 2002-07-17									
; NUMBER OF SEQ ID NOS: 624									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 312									
; LENGTH: 914									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-198-053-312									
Query Match									
100.0%; Score 2321; DB 2; Length 914;									
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									

Best Local Similarity 100.0%; Pred. No. 1.3e-222;									
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	FTHRSSVSTTSGTPTTVILGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG	60						
Db	159	FTHRSSVSTTSGTPTTVILGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG	218						
Qy	61	SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGDAICTHRDPDPTGP	120						
Db	219	SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGDAICTHRDPDPTGP	278						
Qy	121	GLDREQLYLELSOLTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT	180						
Db	279	GLDREQLYLELSOLTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT	338						
Qy	181	INNLRYMADMGQPSGLKFNITDNVWKHLSPLEFQSSSLGARYTGCRRVIALRSVKNGAETR	240						
Db	339	INNLRYMADMGQPSGLKFNITDNVWKHLSPLEFQSSSLGARYTGCRRVIALRSVKNGAETR	398						
Qy	241	VOLLCTVLOPLSGPLPIKOVFHELSSQOHTGITRLGPYSLDKDSLJNGYNEPGDEPPT	300						
Db	399	VOLLCTVLOPLSGPLPIKOVFHELSSQOHTGITRLGPYSLDKDSLJNGYNEPGDEPPT	458						
Qy	301	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKSATFNSTEGVLOHLRL	360						
Db	459	TPKPATTFPLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMKGKSATFNSTEGVLOHLRL	518						
Qy	361	PLFQKSSMGPFYLGCOLISLRPEKOGAATGVTCTTCTYHPDPVPGGLDIOQLYWELSQLTH	420						
Db	519	PLFQKSSMGPFYLGCOLISLRPEKOGAATGVTCTTCTYHPDPVPGGLDIOQLYWELSQLTH	578						
Qy	421	GVTQLGFVYLDRLDSLFG	439						
Db	579	GVTQLGFVYLDRLDSLFG	597						
RESULT 13									
US-10-198-053-478									
; Sequence 478 Application US/10198053									
; Patent No. 6858710									
; GENERAL INFORMATION:									
; APPLICANT: Bangur, Chaitanya S.									
; APPLICANT: Retter, Marc W.									
; APPLICANT: Fanger, Gary R.									
; APPLICANT: Hill, Paul									
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY									
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER									
; FILE REFERENCE: 210121.462C9									
; CURRENT APPLICATION NUMBER: US/10/198,053									
; CURRENT FILING DATE: 2002-07-17									
; NUMBER OF SEQ ID NOS: 624									
; SOFTWARE: FastSeq for Windows Version 4.0									
; SEQ ID NO 478									
; LENGTH: 914									
; TYPE: PRT									
; ORGANISM: Homo sapiens									
US-10-198-053-478									
Query Match									
100.0%; Score 2321; DB 2; Length 914;									
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									

Qy 1 FTHRSSVSTSTGPTGYVLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
|||||
Db 159 FTHRSSVSTSTGPTGYVLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218

Qy 61 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 120
|||||
Db 219 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 278

Qy 121 GLDRQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
|||||
Db 279 GLDRQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

Qy 181 INNLRYMADMGQPGSLKFNITDNVMKHLSPLFORSISLGARYTGCRIALRSVKNGAETR 240
|||||
Db 339 INNLRYMADMGQPGSLKFNITDNVMKHLSPLFORSISLGARYTGCRIALRSVKNGAETR 398

Qy 241 VDLCTYLOPLSGPLIKQVFHELSSQOOTHGITRLGYSLDKDSLNGYNEPGDEPPT 300
|||||
Db 399 VDLCTYLOPLSGPLIKQVFHELSSQOOTHGITRLGYSLDKDSLNGYNEPGDEPPT 458

Qy 301 TPKPATTELPPLSEATTAMGVHLKTLTNFTISNLQYSPDMGKSATFNSTEGVLOHLR 360
|||||
Db 459 TPKPATTELPPLSEATTAMGVHLKTLTNFTISNLQYSPDMGKSATFNSTEGVLOHLR 518

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHDPVPVGPGLDIOQLYWELSQLTH 420
|||||
Db 519 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHDPVPVGPGLDIOQLYWELSQLTH 578

Qy 421 GVTQLGFYVLDROSLFING 439
|||||
Db 579 GVTQLGFYVLDROSLFING 597

RESULT 14
US-09-827-271-312
; Sequence 312, Application US/09827271
; Patent No. 6962980
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 312
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-827-271-312

Query Match 100.0%; Score 2321; DB 2; Length 914;
Best Local Similarity 100.0%; Pred. No. 1.3e-222;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTGPTGYVLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
|||||
Db 159 FTHRSSVSTSTGPTGYVLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 218

Qy 61 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 120
|||||
Db 219 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPGTP 278

Qy 121 GLDRQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
|||||
Db 279 GLDRQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

Qy 181 INNLRYMADMGQPGSLKFNITDNVMKHLSPLFORSISLGARYTGCRIALRSVKNGAETR 240
|||||
Db 339 INNLRYMADMGQPGSLKFNITDNVMKHLSPLFORSISLGARYTGCRIALRSVKNGAETR 398

Qy 241 VDLCTYLOPLSGPLIKQVFHELSSQOOTHGITRLGYSLDKDSLNGYNEPGDEPPT 300
|||||
Db 399 VDLCTYLOPLSGPLIKQVFHELSSQOOTHGITRLGYSLDKDSLNGYNEPGDEPPT 458

Qy 301 TPKPATTELPPLSEATTAMGVHLKTLTNFTISNLQYSPDMGKSATFNSTEGVLOHLR 360
|||||
Db 459 TPKPATTELPPLSEATTAMGVHLKTLTNFTISNLQYSPDMGKSATFNSTEGVLOHLR 518

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHDPVPVGPGLDIOQLYWELSQLTH 420
|||||
Db 519 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHDPVPVGPGLDIOQLYWELSQLTH 578

Qy 421 GVTQLGFYVLDROSLFING 439
|||||
Db 579 GVTQLGFYVLDROSLFING 597

RESULT 15
US-10-198-053-595
; Sequence 595, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 595
; LENGTH: 3451
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 177, 335, 523, 618, 663, 875, 961, 1001, 1441, 1555, 1560,
; LOCATION: 1563, 1574, 1585, 2065, 2070, 2683, 2990, 3269, 3381, 3401
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-198-053-595

Query Match 99.6%; Score 2312; DB 2; Length 3451;
Best Local Similarity 99.8%; Pred. No. 8.8e-221;
Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	2696	FTHRSSVSTTGTCTVYLGASKTPASIFGFSAAASHLLILFTLNFTITNLRAYEENWMPG	2755
Qy	61	SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRPEKDGATGVDAICTHRPDPGTP	120
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Qy	121	GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT	180
Db	2816	GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT	2875
Qy	181	INNRYMADMGPQGSUKFNITDNVMKHLSPLFORSSLGARYTGCVRVIALRSVKNGAETR	240
Db	2876	INNRYMADMGPQGSUKFNITDNVMKHLSPLFORSSLGARYTGCVRVIALRSVKNGAETR	2935
Qy	241	VDLLCTYLQPLSGGGLPIKQVFHELSCQTHGITRLGPISLDKDSLJLNGYNRPGDEPPT	300
Db	2936	VDLLCTYLQPLSGGGLPIKQVFHELSCQTHGITRLGPISLDKDSLJLNGYNRPGDEPPT	2995
Qy	301	TPKPATTELPPLSEATTANGYHLKTLTLNFTISNLOYSMDMGKGSATFNSTEGVLQHLLR	360
Db	2996	TPKPATTELPPLSEATTANGYHLKTLTLNFTISNLOYSMDMGKGSATFNSTEGVLQHLLR	3055
Qy	361	PLFOKSSMGPFYLGCOLISLRAPEKDGATGVDTTCTYHPDPVPGGLDIOQLYWELSOLTH	420
Db	3056	PLFOKSSMGPFYLGCOLISLRAPEKDGATGVDTTCTYHPDPVPGGLDIOQLYWELSOLTH	3115
Qy	421	GVTOGLGVVLDORDSLFING	439
Db	3116	GVTOGLGVVLDORDSLFING	3134

Search completed: June 7, 2007, 17:53:42
Job time : 115 secs

SCORE Search Results Details for Application 10687035 and Search Result 20070607_154735_us-10-687-035-1_copy_14_452.rup.

Score Home	Retrieve Application List	SCORE System Overview	SCORE FAQ	Comments / Suggestions
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This page gives you Search Results detail for the Application 10687035 and Search Result 20070607_154735_us-10-687-035-1_copy_14_452.rup.

[Go Back to previous page](#)

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 7, 2007, 17:45:26 ; Search time 373 Seconds
(without alignments)
1261.830 Million cell updates/sec

Title: US-10-687-035-1_COPY_14_452
Perfect score: 2321
Sequence: 1 FTRHSSVSTSTPGPTVYL.....HGVTOGFVLDLDRDSLFTNG 439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3281787 seqs, 1072124677 residues 3281787

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_8.4.4
1: uniprot_sprot:~
2: uniprot_trembl:~

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2317	99.8	6995	2 Q96RK2_HUMAN	Q96rk2 homo sapien

2	2301	99.1	1148	2	Q9H7S7_HUMAN	Q9h7s7 homo sapien
3	2301	99.1	22152	2	Q8WX17_HUMAN	Q8wx17 homo sapien
4	1512	65.1	867	2	Q6ZQW5_HUMAN	Q6zqw5 homo sapien
5	217	9.3	258	2	Q9D1H1_MOUSE	Q9d1h1 mus musculus
6	117.5	5.1	729	2	Q8DKG0_SYNEL	Q8dkg0 synechococc
7	115.5	5.0	865	2	Q2FN05_METHJ	Q2fnd5 methanospir
8	115	5.0	531	2	Q16X85_AEDAE	Q16x85 aedes aegyp
9	114.5	4.9	1475	1	NUI53_HUMAN	P49790 homo sapien
10	114	4.9	5010	2	Q716A3_9APHY	Q716a3 trametres sp
11	114	4.9	5010	2	Q4MT18_BACCE	Q4mt18 bacillus ce
12	113.5	4.9	1386	2	Q6P5E2_MOUSE	Q6p5e2 mus musculu
13	113	4.9	520	2	Q716A2_9APHY	Q716a2 trametres sp
14	113	4.9	3486	2	Q28LC2_JANSC	Q28lc2 jannaschia
15	112.5	4.8	1625	2	Q6MVD4_NEUCR	Q6mvd4 neurospora
16	112	4.8	1346	2	Q6ZQ24_MOUSE	Q6zq24 mus musculu
17	112	4.8	1597	2	Q3U3D7_MOUSE	Q3u3d7 mus musculu
18	111.5	4.8	593	2	Q21VH2_RHOP2	Q21vh2 rhodospseudo
19	110.5	4.8	1384	2	Q3E1V7_CHLAU	Q3e1v7 chloroflexu
20	110.5	4.8	1390	2	Q8FX84_METMA	Q8fx84 methanosarc
21	110	4.7	519	2	Q51R80_TRAVE	Q51r80 trametres ve
22	109.5	4.7	1045	2	Q76037_HUMAN	Q76037 homo sapien
23	109.5	4.7	1475	2	Q5T917_HUMAN	Q5t917 homo sapien
24	109	4.7	519	1	LAC2_TRAVE	Q12718 trametres ve
25	109	4.7	519	1	LAC2_TRAVI	Q99046 trametres vi
26	109	4.7	519	2	Q50JG5_TRAVE	Q50jg5 trametres ve
27	108.5	4.7	783	2	Q5KMX8_CRYNE	Q5kxm8 cryptococcu
28	108.5	4.7	783	2	Q55X04_CRYNE	Q55x04 cryptococcu
29	108	4.7	519	2	Q96UK8_TRAVE	Q96uk8 trametres ve
30	108	4.7	720	2	Q32DV7_SHIDS	Q32dv7 shigella dy
31	108	4.7	725	2	Q5AJJ5_CANAL	Q5ajj5 candida alb
32	108	4.7	957	2	Q9UKN0_HUMAN	Q9ukn0 homo sapien
33	108	4.7	2281	2	Q5IT20_9CALI	Q5it20 sapovirus s
34	108	4.7	2287	2	Q1E9D6_COCIM	Q1e9d6 coccidioid
35	107.5	4.6	605	2	Q94K06_ARATH	Q94k06 arabidopsis
36	107.5	4.6	944	2	Q9UP82_HUMAN	Q9up82 homo sapien
37	107	4.6	1713	2	Q8TGE1_YEAST	Q8tge1 saccharomyc
38	107	4.6	2520	2	Q4MNM6_BACCE	Q4nm6 bacillus ce
39	106.5	4.6	1227	2	Q301T2_STRSU	Q301t2 streptococc
40	106	4.6	2280	2	Q6XDK9_9CALI	Q6xdk9 sapovirus m
41	105.5	4.5	463	2	Q5EBY5_9APHY	Q5eby5 lentinus ti
42	105.5	4.5	1829	2	Q1FE06_9CHLR	Q1fed6 roseiflexus
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44	105	4.5	493	2	Q6ZNI4_HUMAN	Q6zni4 homo sapien
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ALIGNMENTS

RESULT 1
Q96RK2_HUMAN PRELIMINARY; PRT; 6995 AA.
ID Q36RK2_HUMAN
AC Q96RK2;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2004, sequence version 2.
DE 18-APR-2006, entry version 14.
DE Mucin 16 (Fragment).
GN Name=MUC16;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;

OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] -----
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21347965; PubMed=11369781; DOI=10.1074/jbc.M103554200;
RA Yin B.-W., Lloyd K.O.;
RT "Molecular cloning of the cal25 ovarian cancer antigen. identification
as a new mucin, muc16.";
RL J. Biol. Chem. 276:27371-27375(2001).
RN [2] -----
RP NUCLEOTIDE SEQUENCE.
RA Lloyd K.O., Yin B.-W.T.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
OC EMBL; AF361486; AK74120.3; -; mRNA.
DR HSSP; Q9D1H1; 11VZ.
DR SMR; Q96RK2; 6809-6922.
DR InterPro; IPR000194; ATPase_a_b_n1-bd.
DR InterPro; IPR000082; SEA.
DR Pfam; PF01390; SEA; 21.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00152; ATPASE_ALPHA_BETA; UNKNOWN 1.
DR PROSITE; PS00024; SEA; 6.
FT NON TER 1 1
SQ SEQUENCE 6995 AA; 744966 MW; 80C797DBDBF33A2B CRC64;

Query Match 99.88; Score 2317; DB 2; Length 6995;
Best local Similarity 99.88; Pred. No. 4.7e-165;
Matches 438; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTSGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
DB 6240 FTHRSSVSTTSGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 6299

QY 61 SRKNTTERRVLOGLLRLPKNTSVGLPYSGCRUTLLRPEKDGATGVAICTHRPDPTGP 120
DB 6300 SRKNTTERRVLOGLLRLPKNTSVGLPYSGCRUTLLRPEKDGATGVAICTHRPDPTGP 6359

QY 121 GLDREQYILELSQLTHSITELGPLYTLDRDSLYNGFTHRSSVPTTSTGVWSEEPFTINFT 180
DB 6360 GLDREQYILELSQLTHSITELGPLYTLDRDSLYNGFTHRSSVPTTSTGVWSEEPFTINFT 6419

QY 181 INNLRYVADNGQPGSLKFNITDNVMKLLSPLFORSSILGARYTGCRIALRSVKNGAETR 240
DB 6420 INNLRYVADNGQPGSLKFNITDNVMKLLSPLFORSSILGARYTGCRIALRSVKNGAETR 6479

QY 241 VDLCTYIQLPSGPLPIKQVFEHLSQQTHGITRLGPLYSLDKOSLYANGYNEPGDEPPT 300
DB 6480 VDLCTYIQLPSGPLPIKQVFEHLSQQTHGITRLGPLYSLDKOSLYANGYNEPGDEPPT 6539

QY 301 TKPRTFTLPPLESEATKGYHLKLTILNTINLQYSPDMGKGSATNSTEGVLOHLRL 360
DB 6540 TKPRTFTLPPLESEATKGYHLKLTILNTINLQYSPDMGKGSATNSTEGVLOHLRL 6599

QY 361 PLFQKSSMGPFYLGCOLISLRPEKKGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSOLTH 420
DB 6600 PLFQKSSMGPFYLGCOLISLRPEKKGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSOLTH 6659

QY 421 GVTQGLGYVLDRDSLFLNG 439
DB 6660 GVTQGLGYVLDRDSLFLNG 6678

RESULT 2
Q9H7S7 HUMAN
ID Q9H7S7 HUMAN PRELIMINARY; PRT; 1148 AA.
AC Q9H7S7;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 18-APR-2006, entry version 20.
DE CDNA FLJ14303 f1s, clone PLACE2000132.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1] -----
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Placenta;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Negai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Oshima A., Sasaki N., Arita M., Inose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshihara Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiya Y., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yanazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hara H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
cDNAs.";
RL Nat. Genet. 36:40-45(2004).
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CC Distributed under the Creative Commons Attribution-NoDerivs License
CC -----
OC EMBL; AK04365; BAB14899.1; -; mRNA.
DR HSSP; Q9D1H1; 11VZ.
DR SMR; Q9H7S7; 962-1075.
DR InterPro; IPR000082; SEA.


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DR Pfam: PF01390; SEA; 8.
DR PROSITE: PSS0024; SEA; 3.
SQ SEQUENCE 1148 AA; 127958 MW; 3861B0D5EFD8ABC CRC64;

Query Match          99.1%; Score 2301; DB 2; Length 1148;
Best Local Similarity 99.5%; Pred. No. 6.3e-165;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTHRSVSTSTGCTPTVYLGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENMWPG 60
DB 1 FTHRSVSTSTGCTPTVYLGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENMWPG 452
QY 61 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 120
DB 61 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 512
QY 121 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSGVWVEEPFTLNFT 180
DB 121 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSGVWVEEPFTLNFT 572
QY 513 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSGVWVEEPFTLNFT 572
DB 513 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSGVWVEEPFTLNFT 572
QY 181 INNLRYMADMGQPSGLKFNITDNVVKHLLSPFORSSLGARYTGCVRVIALRSVKNGAETR 240
DB 181 INNLRYMADMGQPSGLKFNITDNVVKHLLSPFORSSLGARYTGCVRVIALRSVKNGAETR 632
QY 241 VDLCTYIQLPLSGGGLPIKQVFHELSSQTHGITRLGPIYSLDKDSLILYNGYNEPGDEPPT 300
DB 241 VDLCTYIQLPLSGGGLPIKQVFHELSSQTHGITRLGPIYSLDKDSLILYNGYNEPGDEPPT 692
QY 301 TPKPATTELPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
DB 301 TPKPATTELPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 752
QY 361 PLFKSKSGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 420
DB 361 PLFKSKSGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 812
QY 421 GVTQLGFYVLDRLSLFING 439
DB 421 GVTQLGFYVLDRLSLFING 831

RESULT 3
Q8WX17.HUMAN PRELIMINARY; PRT; 22152 AA.
AC Q8WX17;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2003, sequence version 2.
DT 13-JUN-2006, entry version 18.
DE Ovarian cancer related tumor marker CA125.
GN Name=WUC16;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21646939; PubMed=11786729; DOI=10.1159/000050638;
RA O'Brien T.J., Beard J.B., Underwood L.J., Dennis R.A., Santin A.D.,
RA York L.;
RT "The CA 125 gene: an extracellular superstructure dominated by repeat
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sequences.";
RL Tumour Biol. 22:348-366(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA O'Brien T.J., Underwood L.J., Beard J.B.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR ENBL: AF414442; AAL65133.2; -; mRNA.
DR SMR; Q8WX17; 21966-22079.
DR Ensembl; ENSG00000181143; Homo sapiens.
DR HGNC; HGNC:15582; MUC16.
DR GO; GO:0019898; C:extrinsic to membrane; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; NAS.
DR InterPro; IPR000194; ATPase_a_b_n1-bd.
DR Pfam; PF01390; SEA; 56.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PSS00152; ATPASE_ALPHA_BETA; UNKNOWN_1.
DR PROSITE; PSS0024; SEA; 11.
SQ SEQUENCE 22152 AA; 2353428 MW; B3E7B0F19997A440 CRC64;

Query Match          99.1%; Score 2301; DB 2; Length 22152;
Best Local Similarity 99.5%; Pred. No. 3.7e-163;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTHRSVSTSTGCTPTVYLGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENMWPG 60
DB 21397 FTHRSVSTSTGCTPTVYLGASKTPASIFGSPASASHLLILFTLNFTITNLRYEENMWPG 21456
QY 61 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 120
DB 61 SRKENTTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 21516
QY 121 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSGVWVEEPFTLNFT 180
DB 121 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSGVWVEEPFTLNFT 21576
QY 181 INNLRYMADMGQPSGLKFNITDNVVKHLLSPFORSSLGARYTGCVRVIALRSVKNGAETR 240
DB 181 INNLRYMADMGQPSGLKFNITDNVVKHLLSPFORSSLGARYTGCVRVIALRSVKNGAETR 21636
QY 241 VDLCTYIQLPLSGGGLPIKQVFHELSSQTHGITRLGPIYSLDKDSLILYNGYNEPGDEPPT 300
DB 241 VDLCTYIQLPLSGGGLPIKQVFHELSSQTHGITRLGPIYSLDKDSLILYNGYNEPGDEPPT 21696
QY 301 TPKPATTELPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
DB 21697 TPKPATTELPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 21756
QY 361 PLFKSKSGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 420
DB 21757 PLFKSKSGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 21816
QY 421 GVTQLGFYVLDRLSLFING 439
DB 21817 GVTQLGFYVLDRLSLFING 21835
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RESULT 4
Q6ZQW5_HUMAN
ID Q6ZQW5_HUMAN PRELIMINARY; PRT; 867 AA.
AC Q6ZQW5_
DT 03-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 18-APR-2006, entry version 9.
DE CDNA FLJ46845 fis, clone UTERU3001946, highly similar to Homo sapiens
DE mucin 16 (MUC16).
DE
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Uterus;
RA Suzuki O., Sasaki N., Aotsuka S., Shoji T., Ichihara T., Shiohata N.,
RA Matsumoto K., Hirano M., Sano S., Nomura R., Yoshikawa Y.,
RA Matsumura Y., Mochiya S., Chiba E., Momiyama H., Onogawa S.,
RA Kaeriyama S., Satoh N., Matsunawa H., Takahashi E., Kataoka R.,
RA Kuga N., Kuroda A., Satoh I., Kanata K., Takami S., Terashima Y.,
RA Watanabe M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A.,
RA Ishii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
RA Kimura K., Yamashita H., Matsumoto K., Nakamura Y., Sekine M.,
RA Kikuchi H., Kanda K., Wagatsuma M., Murakawa K., Kanehori K.,
RA Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B., Suzuki Y.,
RA Sugano S., Nagahara K., Masuo Y., Nagai K., Isogai T.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AK128681; BAC87568.1; -; mRNA.
DR InterPro; IPR000082; SEA.
DR Pfam; PF01390; SEA; 6.
DR PROSITE; PS50024; SEA; 2.
SQ SEQUENCE 867 AA; 96201 MW; C7B303258839622 CRC64;

Query Match 65.1%; Score 1512; DB 2; Length 867;
Best Local Similarity 94.8%; Pred. No. 2.4e-105;
Matches 291; Conservative 5; Mismatches 3; Indels 8; Gaps 1;

QY 1 FTHRSSVSTTPTGTPVYLGASKTPASIFGPSAASHLLILFLNFTITNLRYENMWPG 60
DB 569 FTHRSSVSTTPTGTPVYLGASKTPASIFGPSAASHLLILFLNFTITNLRYENMWPG 628

QY 61 SRKFNTERVQLGILLRPLFNKTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDTGP 120
DB 629 SRKFNTERVQLGILLRPLFNKTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDTGP 688

QY 121 GLDREQLYELSLQTHSITELGPTYLDRSLYNGFTHRSSVPTTSGVSVSEPTFLNFT 180
DB 689 GLDREQLYELSLQTHSITELGPTYLDRSLYNGFTHRSSVPTTSGVSVSEPTFLNFT 748

QY 181 INNLRYMDMDQPGSLKFNITDNWKHLLSPILFQRSSILGARYTGCRTVALRSVKNGAETR 240
DB 749 INNLRYMDMDQPGSLKFNITDNWKHLLSPILFQRSSILGARYTGCRTVALRSVKNGAETR 808
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QY 241 VDLCTTYLQPLSGPLPIKQVTHELSQOHTGLRGLPSYLDKDSLYLNGYNEPGDPPT 300
DB 809 VDLCTTYLQPLSGPLPIKQVTHELSQOHTGLRGLPSYLDKDSLYLNGHH-----T 860

QY 301 TPKPATY 307
DB 861 LQRQSTT 867

RESULT 5
QSDIHI_MOUSE
ID QSDIHI_MOUSE PRELIMINARY; PRT; 258 AA.
AC QSDIHI;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 30-MAY-2006, entry version 24.
DE 18-day embryo whole body cDNA, RIKEN full-length enriched library,
DE clone:111008114 product:hypothetical SEA domain containing protein,
DE full insert sequence.
GN Name=111008114rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-5;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Methods Enzymol. 303:19-44(1999).
RN [2]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141072; DOI=10.1126/science.1112014;
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Altanis V., Allen J.E.,
RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hilt D., Humintek L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasaki Y., Kelso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Farzi S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavai G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Ring J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
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RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Varado R., Wei C.L., Yagi K.,
RA Yamaniishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusuc V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Ida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.,
RA "The transcriptional landscape of the mammalian genome.";
RL Science 309:1559-1563(2005).
RN [3]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX PubMed=16141073; DOI=10.1126/science.1112009;
RG RIKEN Genome Exploration Research Group, and Genome Science Group
RT (Genome Network Core Team) and the FANTOM Consortium;
RT "Antisense Transcription in the Mammalian Transcriptome.";
RL Science 309:1564-1566(2005).
RN [4]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=22334683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamahata H., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusuc V., Clothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.B.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lennhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Saro K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume M., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Sasaki D., Shibata K., Shinagawa A.,
RA Birney E., Hayashizaki Y.,
RA "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [5]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/3505500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., De Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RA "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [6]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagasaki S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamanoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipillar sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
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RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
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RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [9]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [9]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [9]
RN NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.,
RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.


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Db 651 LLAUPTIAVLAEPE--SYGVOELVDQRLORCTPEQLKIFILGSK-----GNYOG 699
Oy 391 VDTCTYHPDPVGPGLDIIQQLYWEISQLTHGVTQL 425
Db 700 VD---RYIPLPIHPESFLO-----QVTGLTSL 724

RESULT 7
O2FND5 METHJ
ID O2FND5 METHJ PRELIMINARY; PRT; 865 AA.
AC O2FND5
DT 21-MAR-2006, integrated into UniProtKB/TrEMBL.
DT 11-JUL-2006, entry version 4.
DE PKD.
GN OrderedLocusNames=Mhuh_2522;
OS Methanospirillum hungatei (strain JF-1 / DSM 864).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanomicrobiales;
OC Methanospirillaceae; Methanospirillum.
OX NCBI_TaxID=323259;
RN [1]
RP NUCLEOTIDE SEQUENCE (LARGE SCALE GENOMIC DNA).
RG US DOE Joint Genome Institute;
RA Capeland A., Lucas S., Lapidus A., Barry K., Dettler J.C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Brettin T., Bruce D., Han C.,
RA Tapia R., Gilna P., Kiss H., Schmutz J., Larimer F., Land M.,
RA Kyrides N., Ivanova N., McInerney M.J., Brockman F., Culley D.,
RA Ferry J.G., Gunsalus R.P., Morrison M., Plugge C., Scholten J.,
RA Stams A.J.M., Boone D.R., Richardson P.;
RT "Complete sequence of Methanospirillum hungatei JG-1.";
RL Submitted (JAN-2006) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CP000254; AB042222.1; -; Genomic DNA.
DR GenomeReviews; CP000254.GR; Mhuh_2522.
DR InterPro; IPR000601; PKD.
DR Pfam; PF00801; PKD; 5.
DR SMART; SM00089; PKD; 8.
DR PROSITE; PS00093; PKD; 8.
KW Complete proteome.
SQ SEQUENCE 865 AA; 95487 MW; 9841DEC0B9217191 CRC64;
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Query Match 5.0%; Score 115.5; DB 2; Length 865;
Best Local Similarity 20.7%; Pred. No. 13;
Matches 74; Conservative 56; Mismatches 132; Indels 95; Gaps 18;

Oy 24 KTPASIFGSAASHLLIIFTLN---FTTNURVEENWFGSRKNTERTVLAQGLRLPK 80
Db 11 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
257 KSPVCHYPERGLYTSMTYITIDGAPYITITKNRYLKYVPAGTDFATP--VEG----- 307

Oy 81 NTSVGPL---YSCRLTLLRPEXGDE-----ATGVDAICTHRDPD*GGLDRSQLYLEL 131
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
308 ---IAPLCVAYS-----VINPTOSWEFNFGDNSTATSAQATHCYGTSN-----YF 350

Oy 132 SOUTHSITEAGPYLDRLOSNGFTHRSSVPTTSTGVVSEEPFTLNFTINLRYPADWG 191
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
351 PSITCYSCNNLCDTVEGKEPIIV----HQPRILIAQGSALNEYKEFTD-APEGLKYSWDG 405
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Oy 192 Q-----PGSLKFNITDNVKKHLLSPLFQRSSLGARYT--GCRVIALRSVKNGAETRVDL 243
Db 406 DGTRAEGPAPSHRFDMEGT-----YRVSLLVVTGTCGNAIAVKELMKPKGLDF 455
Oy 244 LCTYLQPLSG-----PGLPTKQVH-----ELSQOT---HGITRLGPGYSLDKDS 284
Db 456 TAT---PLAGCAPHCVOFNKSPFELPSLRVWDFGDSSTSEKNPFCHCFRPGPYVTUTD 512
Oy 285 LYLNGVNEPGDEPPT---TPKPATTFPLPSEATTAMGYHLKTLTLTNFTNISLQVYS 338
Db 513 TFPNGTQCEVKENYITAHAVEKPSFTMFPHGDA-----PLTVKFTDITVDYA 560

RESULT 8
O16X85 AEDAE
ID O16X85 AEDAE PRELIMINARY; PRT; 531 AA.
AC O16X85
DT 25-JUL-2006, integrated into UniProtKB/TrEMBL.
DT 25-JUL-2006, sequence version 1.
DE Hypothetical protein.
DE Hypothetical protein.
GN ORFNames=AaeL_AAE1008949;
OS Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Culicidae;
OC Culicinae; Culicini; Aedes; Stegomyia.
RN NCBI_TaxID=7159;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Liverpool;
RG The Broad Institute Genome Sequencing Platform;
RA Loftus B.J., Nene V.M., Wortman J.R., Severson D.W., Collins F.,
RA Galagan J., Devon K., Henn M.R., Jaffe D., Rounsley S., DeCaprio D.,
RA Kodira C., Lander E., Crawford M., Hannick L.I., Bidwell S., Haas B.,
RA Amedeo P., Orvis J., White O.R., Shumway M., Koo H., Zhao Y.,
RA Holmes M., Miller J., Schatz M., Pop M., Salzberg S., Pal G.,
RA Utterback T., Rogers Y.-H., Kravitz S., Butler J., Alvarez P.,
RA Gnerre S., Grabherr M., Kleber M., Mauceli E., Brockman M., Young S.,
RA LaButti K., Pushparaj V., Koehrsen M., Engels R., Montgomery P.,
RA Pearson M., Howarth C., Zeng O., Yandava C., O'Leary S., Alvarado L.,
RA Nusbaum C., Birren B., Fraser C.M.;
RT "The Genome Sequence of Aedes aegypti (strain Liverpool).";
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Liverpool;
RA Loftus B.J., Nene V.M., Hannick L.I., Bidwell S., Haas B., Amedeo P.,
RA Orvis J., Wortman J.R., White O.R., Salzberg S., Shumway M., Koo H.,
RA Zhao Y., Holmes M., Miller J., Schatz M., Pop M., Pal G.,
RA Utterback T., Rogers Y.-H., Kravitz S., Fraser C.M.;
RL Submitted (OCT-2005) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; CH477545; EAT39234.1; -; Genomic DNA.
KW Hypothetical protein.
SQ SEQUENCE 531 AA; 56921 MW; F9BA04611ABF2350 CRC64;
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Query Match 5.0%; Score 115; DB 2; Length 531;
Best Local Similarity 23.0%; Pred. No. 7.5;


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Db 455 AFVASKPKEEEMVPLPKISLPITS-----SSLPTNFSSPEITTSPPSPINSQALTN 510
Qy 184 LRYMDMGQPGSLKFNITDNVKKHLLSPLFORSSILGARYTGCRVIALRSVKNKAETRVDL 243
    || | : : || : : || : | : || : | : || : | : || : | : || : | :
Db 511 KVQMTSPSTGSPFKESSPIVKSTEANVLPPSSIG--FTFSVPVAKTAELSGSSST--- 565
Qy 244 LCTYLOPLSGPLPIKOVFHELSSQOHTHITRL-----GPY---SLDKDSLY 286
    || : | : || : | : || : | : || : | : || : | : || : | : || : | :
Db 566 ----LEPI-----ISSAHVTTVNSTNCKTKPPEDCEGFPFAELILKGSV 608
Qy 287 LINGNERGDEP-----PTTPKPATTFPLPSEATTANGVHLKTLTLNFTISNLQYS 338
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 609 LDILKSGFASPKIDSVAAGPTATSPVVYTREAIS-----SFSSSGIGFG 653
Qy 339 PDMGKGSATFNSTEGVLOHLLRPLFOKSMGPYILGCOLISLRPEKOGAATGVDT 393
    : || : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 654 ESLKAGSSWOCDT-----CLLQNKVTDNKKIACQAKLSPRDTAKQTGIET 699

RESULT 10
ID Q716A3_9APHY PRELIMINARY; PRT; 520 AA.
AC Q716A3;
DT 05-JUN-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
DT 18-APR-2006, entry version 14.
DE Laccase.
GN Name=poxl;
OS Trametes sp. I-62.
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Aphyllophorales; Trametes.
OX NCBI_TaxId=51095;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=i-62;
RX MEDLINE=2833033; PubMed=12951799;
RA Gonzalez T., del Carmen Terton M., Zapico E., Yague S., Tellez A.,
RA Junca H., Gonzalez A.;
RT "Identification of a new laccase gene and confirmation of genomic
RT predictions by cDNA sequences of Trametes sp. I-62 Laccase family.";
RL Mycol. Res. 107:727-735(2003).
CC -----
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CC -----
DR EMBL: AF548032; AAO12267.1; -; mRNA.
DR HSSP: Q9Y780; 1A65.
DR SMR: Q716A3; 22-519.
DR GO: GO:0005507; F:coppper ion binding; IEA.
DR GO: GO:0046872; F:metal ion binding; IEA.
DR GO: GO:0016491; F:oxidoreductase activity; IEA.
DR InterPro: IPR001117; Cu-oxidase.
DR InterPro: IPR011706; Cu-oxidase 2.
DR InterPro: IPR011707; Cu-oxidase 3.
DR InterPro: IPR002355; Cu-oxidase_Cu_BS.
DR InterPro: IPR008972; Cupredoxin.
DR Pfam: PF00394; Cu-oxidase; 1.
DR Pfam: PF07731; Cu-oxidase 2; 1.
DR Pfam: PF07732; Cu-oxidase 3; 1.
DR PROSITE: PS00079; MULTICOPPER_OXIDASE1; 1.
KW Copper; Metal-binding; Oxidoreductase; Repeat.
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SQ SEQUENCE 520 AA; 55915 MW; 0C33786ABE7BD8CD CRC64;
Query Match 4.9%; Score 114; DB 2; Length 520;
Best Local Similarity 20.0%; Pred. No. 8.7;
Matches 70; Conservative 46; Mismatches 124; Indels 110; Gaps 16;

Qy 116 DPTGP-----GLDREQLYLELSQTHSITELGP--YTLDRDSLYVNGFTHRSSVPTTSTGV 169
    || | : | : || : | : || : | : || : | : || : | : || : | : || : | :
Db 149 DPLDPAFRYDVDDSTVITLSDWYHTAARUGPRFLPGADATLINGLGRSSSTPTANVT 208
    || : | : || : | : || : | : || : | : || : | : || : | : || : | :
Qy 170 VS-----EEFTLN-----FTNNLRYMDMGQPGS 195
    : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 209 INVQHGKRYRFLVSLSCDPNHTFSIDGHNITVIEVDGVNSKPLTVDSIQIFA--AORYS 266
Qy 196 LKFNITDNVKKHLL--SPLFORSSLGA-----RYTGCRVIALRSVKNKAETRVDL 246
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 267 FVLNANTQVGNWIRANPNFGTTGFAGGINSAILRYOGAPIIEPTVQ--TTSVIPLVET 324
Qy 247 YLQPLSG---PGLPIKQVFHELSSQOHTHITRLGYPYSLDKD---SLYLINGYN---EPGPDE 297
    || | : | : || : | : || : | : || : | : || : | : || : | : || : | :
Db 325 NLHPLVPTIVPGLPVSG-----GVDKAINLAFNFGNFFINNATET 366
Qy 298 PFTTP-----KPATTELPPLS-----EATTAMGYHLKTLTL-----NTTISNLQYS 338
    || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 367 PPTVPVLLQILSGASTAQDILLPGSVYPLPAHSSIEITLPATTLAAGAPHPHLLGHVFA 426
Qy 339 PDMGKGSATFNSTEGVLOHLLRP-----LFKSSMGPYILGCOL 377
    || : | : | : : : : : : : : : : : : : : : : : : : : : : :
Db 427 VVRSAGSTAINVYDFIRDVVSTGTPAAGDNVIRFHTDTPGPWELHCHI 476

RESULT 11
Q4MT18_BACCE
ID Q4MT18_BACCE PRELIMINARY; PRT; 5010 AA.
AC Q4MT18;
DT 02-AUG-2005, integrated into UniProtKB/TrEMBL.
DT 02-AUG-2005, sequence version 1.
DT 27-JUN-2006, entry version 7.
DE Cell surface protein.
GN ORFNames=BCE.G9241.1620;
OS Bacillus cereus G9241.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
OC Bacillus cereus group.
OX NCBI_TaxId=269801;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=G9241;
RX PubMed=15155910; DOI=10.1073/pnas.0402414101;
RA Hoffmaster A.R., Ravel J., Rasko D.A., Chapman G.D., Chute M.D.,
RA Marston C.K., De B.K., Sacchi C.T., Fitzgerald C., Mayer L.W.,
RA Maiden M.C.J., Priest F.G., Barker M., Jiang L., Cer R.Z.,
RA Rilstone J., Peterson S.N., Weyant R.S., Galloway D.R., Read T.D.,
RA Popovic T., Fraser C.M.;
RT "Identification of anthrax toxin genes in a Bacillus cereus associated
RT with an illness resembling inhalation anthrax.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:8449-8454(2004).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; AAEK01000008; EAL15315.1; -; Genomic DNA.
DR GO; GO:0005727; C:extrachromosomal circular DNA; IEA.
DR GO; GO:0001525; P:angiogenesis; IEA.
DR GO; GO:0003034; P:cell differentiation; IEA.
DR InterPro; IPR000850; Adenylate kin.
DR InterPro; IPR000194; ATPase a_b_n1-bd.
DR InterPro; IPR013320; ConA like subgrp.
DR InterPro; IPR011048; Cyt cdl_haem_C.
DR InterPro; IPR001434; DUF11.
DR Pfam; PF01345; DUF11; 27.
DR TIGRFAMs; TIGR01451; B_ant_repeat; 35.
DR PROSITE; PS00113; ADENYLATE KINASE; UNKNOWN 1.
DR PROSITE; PS00152; ATPASE ALPHA BETA; UNKNOWN 1.
KW Angiogenesis; Differentiation; Proteoglycan.
SQ SEQUENCE 5010 AA; 521891 MW; B00914651BF832DD CRC64;

Query Match 4.9%; Score 114; DB 2; Length 5010;
Best Local Similarity 18.9%; Pred. No. 2e+02;
Matches 88; Conservative 66; Mismatches 155; Indels 156; Gaps 21;

Qy 6 SVSTSTP-----GPTVYLGAASKTPASIFGSPSAASHLLILFTLTIINLRYENWPG 60
Db 3662 TITKTSNFTVDIGTILYISEVKNIGNV-----DAINIIFT-----DSIPA 3703
Qy 61 SRKENTERVLOGLLRP---LFRKNTSVGLYSGCRLLTL-----RPEKDGATG-VDAI 110
Db 3704 GTTFVDPDSVTINGVLOPDTNPENGISIGTIPNSKXILFQVQTNRPPTETEIWNQSSAM 3763
Qy 111 CTRHPDPFGGLDR-----EQYLELSQ---LTHSITELGFPYT 145
Db 3764 YQVSIPTAPPNRSATSNIVTTSLOANIIISKQADVTFVSIQONITVNTLQNIQTVP 3823
Qy 146 LD-----RSLYNGFTHRSSVP---TTSTGVVSEEPFTLTINNLRYM 187
Db 3824 ANNTLFDINPEGTIFIEDLSINNVQIGANPENGITLGTIQDFEIVTISFQVLTSI- 3882
Qy 188 ADMGPGSLKFTINDVKKHL---SPLPORSSILGARYT---GCRVIALRVKNGAETR 240
Db 3883 ----PPGNTVINISDTSYEQIESPPIIQRSLNSNAVTEVRTANVSALKSA-NRSITR 3937
Qy 241 VDLCTYLIQPLSGPG-LPIKQVHELSDQGTITRLGPGYSKDLKSLYNGYNEPGDPEPP 299
Db 3938 IGGIITYTVAVTNAGTVPTWTL--LIDAIAGTTFIPNSILVDGI-----PRPNENP 3988
Qy 300 TT-----PKPATIFLPLSEATTA 318
Db 3989 ITGITLILNPNNTLIVTFQNVVVSIPPNINNIINIAVIHYEQDPS---LPPISETTSS 4045
Qy 319 MGYHLK-----TLTLNFTISNLQSPD-----MGKSATFNS 350
Db 4046 NTFNIQIFDAILIATKSANTILANIDEITYTLVIQNNGSITTNS 4090

RESULT 12
ID Q6P5E2 MOUSE PRELIMINARY; PRT; 1386 AA.
AC Q6P5E2
DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 05-JUL-2004, sequence version 1.
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DT 04-APR-2006, entry version 16.
DE RIKEN CDNA D930015E06.
GN Name=D930015E06Rik;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
[1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6; TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC062940; AAH62940.1; -; mRNA.
DR UniGene; Mm.28836; -.
DR Ensembl; ENSMUSG00000033767; Mus musculus.
DR MGI; MGI:2443399; D930015E06Rik.
SQ SEQUENCE 1386 AA; 152723 MW; 6FCE903EF167E372 CRC64;

Query Match 4.9%; Score 113.5; DB 2; Length 1386;
Best Local Similarity 20.7%; Pred. No. 36;
Matches 113; Conservative 63; Mismatches 170; Indels 201; Gaps 25;

Qy 59 PGRKKNFTTTERVLOGLLRPLFKN----TSVGLYSGCRLLTLRPEKDEATGVDAIC--- 111
Db 300 PGCWNIFSLKLVKGVNLVNTFNVTNTGALFAIPLOIFSAPTKEG-SIGFEVLAHCG 358
Qy 112 ----THRPDPFGGLDRQOLYLELSQLTSHI--TELGPYTLDRDLSLYNG----- 155
Db 359 MHVFMGKSKTENPNWERS---LSLDRSTWMDSELANKLYERWKYKSGDACRRNVLGNS 415
Qy 156 ---FTHRS--SVPTTS--TGVVSEEPFTLTINNLRYMA-----DKGPGCSJ---- 196
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Db	468	ILPSG----	SSSAPFVTNLSAPLTGPTGSSTTGSVTS-----	QESSLSVPIPI	513
Oy	373	LGCQLISLRPEKGAATG-----	VDTTCTYHPD-----	PVGP	405
Db	514	NSSEII---	PSSTGAGLGSSMLPASSTIPVSSTYNLSSSSTVP	IGTG	559

Search completed: June 7, 2007, 17:51:41
Job time : 375 secs

SCORE 2.0 BuildDate: 12/05/2005

SCORE Search Results Details for Application 10687035 and Search Result 20070607_154750_us-10-687-035-1_copy_14_452.rapbn.

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OM protein - protein search, using sw model
Run on: June 7, 2007, 17:57:54 ; Search time 313 Seconds
(without alignments)
478.070 Million cell updates/sec

Title: US-10-687-035-1_COPY_14_452
Perfect score: 2321
Sequence: 1 FTHRSSVSTTPTCTPTVYL.....HGVTQLGFVLDKDSLEIFNG 439

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1387086 seqs, 340856542 residues
Total number of hits satisfying chosen parameters: 1387086

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /EMC_Celeerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB pep.*
2: /EMC_Celeerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB pep.*
3: /EMC_Celeerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB pep.*
4: /EMC_Celeerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
5: /EMC_Celeerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB pep.*
6: /EMC_Celeerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB pep.*
7: /EMC_Celeerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB pep.*
8: /EMC_Celeerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2317	99.8	811	7	US-11-066-316A-961	Sequence 961, App
2	2317	99.8	811	7	US-11-066-316A-965	Sequence 965, App
3	2317	99.8	1890	7	US-11-582-861-6592	Sequence 6592, Ap
4	2317	99.8	13888	7	US-11-066-316A-963	Sequence 963, App
5	2311	99.6	1890	7	US-11-443-428A-775223	Sequence 775223,
6	2301	99.1	1148	6	US-10-475-117-48	Sequence 48, Appl
7	2301	99.1	1148	6	US-10-917-503-18865	Sequence 18865, A
8	2301	99.1	1148	7	US-11-105-233-195	Sequence 195, App
9	2301	99.1	1148	7	US-11-226-554-129	Sequence 129, App
10	2301	99.1	1148	7	US-11-248-718-129	Sequence 129, App
11	2301	99.1	1148	7	US-11-538-552-129	Sequence 129, App
12	2301	99.1	2248	6	US-10-475-117-50	Sequence 50, Appl
13	2301	99.1	9799	6	US-10-475-117-146	Sequence 146, App
14	2301	99.1	11721	6	US-10-475-117-162	Sequence 162, App
15	2301	99.1	22152	6	US-10-544-944-1	Sequence 1, Appl
16	2301	99.1	22152	6	US-10-475-117-315	Sequence 315, App
17	2301	99.1	22152	7	US-11-582-861-6593	Sequence 6593, Ap
18	2205.5	95.0	1307	6	US-10-777-288A-3696	Sequence 3696, Ap
19	2185	94.1	1647	6	US-10-777-288A-3700	Sequence 3700, Ap
20	2005.5	86.4	1832	7	US-11-443-428A-775224	Sequence 775224,
21	1512	65.1	867	6	US-10-777-288A-3863	Sequence 3863, Ap
22	1384.5	59.7	909	7	US-10-475-117-69	Sequence 69, Appl
23	1383.5	59.6	999	7	US-11-443-428A-775226	Sequence 775226,
24	1365.5	58.8	1366	6	US-10-475-117-47	Sequence 47, Appl
25	1348.5	58.1	780	6	US-10-475-117-159	Sequence 159, App
26	1348.5	58.1	780	6	US-10-475-117-158	Sequence 158, App
27	1322	57.0	780	6	US-10-475-117-158	Sequence 71, Appl
28	1317	56.7	594	6	US-10-475-117-71	Sequence 960, App
29	1314.5	56.6	12704	7	US-11-066-316A-960	Sequence 964, App
30	1314.5	56.6	12756	7	US-11-066-316A-964	Sequence 959, App
31	1314.5	56.6	12759	7	US-11-066-316A-959	Sequence 78, Appl
32	1303	56.1	597	6	US-10-475-117-78	Sequence 70, Appl
33	1284.5	55.3	525	6	US-10-475-117-80	Sequence 80, Appl
34	1250.5	53.9	479	6	US-10-475-117-80	Sequence 161, App
35	1242.5	53.5	468	6	US-10-475-117-161	Sequence 962, App
36	1214	52.3	12622	7	US-11-066-316A-962	Sequence 42, Appl
37	1181.5	50.9	443	6	US-10-475-117-42	Sequence 39, Appl
38	1159	49.9	439	6	US-10-475-117-39	Sequence 38, Appl
39	1112	47.9	420	6	US-10-475-117-38	Sequence 79, Appl
40	1112	47.9	420	6	US-10-475-117-79	Sequence 37, Appl
41	1110	47.8	438	6	US-10-475-117-37	Sequence 40, Appl
42	1080	46.5	424	6	US-10-475-117-40	Sequence 72, Appl
43	1080	46.5	424	6	US-10-475-117-72	Sequence 44, Appl
44	1076	46.4	442	6	US-10-475-117-44	Sequence 36, Appl
45	1066	45.9	386	6	US-10-475-117-36	

ALIGNMENTS

RESULT 1
US-11-066-316A-961
; Sequence 961, Application US/11066316A
; Publication No. US20070059710A1
; GENERAL INFORMATION:
; APPLICANT: Luke, May

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STROKE, METHODS OF
; FILE REFERENCE: CL001585
; CURRENT APPLICATION NUMBER: US/11/066, 316A
; CURRENT FILING DATE: 2005-02-25
; NUMBER OF SEQ ID NOS: 55503
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 961
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-066-316A-961

Query Match 99.8%; Score 2317; DB 7; Length 811;
Best Local Similarity 99.8%; Pred. No. 3e-179;
Matches 438; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGSPAASHLLILFTLNFTITNLRYEENWMPG 60
Db 56 FTHRSSVSTTSGTPTVYLGASKTPASIFGSPAASHLLILFTLNFTITNLRYEENWMPG 115
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPTGP 120
Db 116 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPTGP 175
Qy 121 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 176 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 235
Qy 181 INNLRYADMQPGSLKENITDNVMQHLLSPLFORSSLGARYTGCRVIALRSVKNGAETR 240
Db 236 INNLRYADMQPGSLKENITDNVMQHLLSPLFORSSLGARYTGCRVIALRSVKNGAETR 295
Qy 241 VDLICTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT 300
Db 296 VDLICTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT 355
Qy 301 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLOYSPODMKGSATFSTEGVLQHLRL 360
Db 356 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLOYSPODMKGSATFSTEGVLQHLRL 415
Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
Db 416 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 475
Qy 421 GVTOLGFYVLDRODSLFING 439
Db 476 GVTOLGFYVLDRODSLFING 494

RESULT 2
US-11-066-316A-965
; Sequence 965, Application US/11066316A
; Publication No. US20070059710A1
; GENERAL INFORMATION:
; APPLICANT: Luke, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STROKE, METHODS OF
; FILE REFERENCE: CL001585
; CURRENT APPLICATION NUMBER: US/11/066, 316A
; CURRENT FILING DATE: 2005-02-25

; NUMBER OF SEQ ID NOS: 55503
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 965
; LENGTH: 811
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-066-316A-965

Query Match 99.8%; Score 2317; DB 7; Length 811;
Best Local Similarity 99.8%; Pred. No. 3e-179;
Matches 438; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGSPAASHLLILFTLNFTITNLRYEENWMPG 60
Db 56 FTHRSSVSTTSGTPTVYLGASKTPASIFGSPAASHLLILFTLNFTITNLRYEENWMPG 115
Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPTGP 120
Db 116 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPTGP 175
Qy 121 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 176 GLDREQLYLELSQTHSITELGPTYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 235
Qy 181 INNLRYADMQPGSLKENITDNVMQHLLSPLFORSSLGARYTGCRVIALRSVKNGAETR 240
Db 236 INNLRYADMQPGSLKENITDNVMQHLLSPLFORSSLGARYTGCRVIALRSVKNGAETR 295
Qy 241 VDLICTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT 300
Db 296 VDLICTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT 355
Qy 301 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLOYSPODMKGSATFSTEGVLQHLRL 360
Db 356 TPKPATTFPLPSEATTAMGYHLKTLTNFTISNLOYSPODMKGSATFSTEGVLQHLRL 415
Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
Db 416 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 475
Qy 421 GVTOLGFYVLDRODSLFING 439
Db 476 GVTOLGFYVLDRODSLFING 494

RESULT 3
US-11-582-861-6592
; Sequence 6592, Application US/11582861
; Publication No. US20070099251A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Hui
; APPLICANT: Aebersold, Rudolf H.
; TITLE OF INVENTION: TISSUE- AND SERUM-DERIVED GLYCOPROTEINS
; FILE REFERENCE: 460092.404
; CURRENT APPLICATION NUMBER: US/11/582,861
; CURRENT FILING DATE: 2006-10-17
; PRIOR APPLICATION NUMBER: US 60/728,044
; PRIOR FILING DATE: 2005-10-17
; NUMBER OF SEQ ID NOS: 14918
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 6592
; LENGTH: 1890
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-582-861-6592

Query Match      99.8%; Score 2317; DB 7; Length 1890;
Best Local Similarity 99.8%; Pred. No. 8.9e-179;
Matches 438; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||
Db 1135 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 1194

Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 120
    |||
Db 1195 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 1254

Qy 121 GLDREQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||
Db 1255 GLDREQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 1314

Qy 181 INNLRYMADMGPQGSLSKENITDNVMQHLLSPLFQSSSLGARTGCRVIALRSVKNGAETR 240
    |||
Db 1315 INNLRYMADMGPQGSLSKENITDNVMQHLLSPLFQSSSLGARTGCRVIALRSVKNGAETR 1374

Qy 241 VDLCTYLOPLSGPGLPIKQVFHELSSQOOTHGITRLGYPYSLDKDSLYLNGYNPEGPDEPPT 300
    |||
Db 1375 VDLCTYLOPLSGPGLPIKQVFHELSSQOOTHGITRLGYPYSLDKDSLYLNGYNPEGPDEPPT 1434

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMKSGSATFNSTEGVLQHLRL 360
    |||
Db 1435 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMKSGSATFNSTEGVLQHLRL 1494

Qy 361 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVTCTYHPDPVPGGLDIQOLYLWELSOLTH 420
    |||
Db 1495 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVTCTYHPDPVPGGLDIQOLYLWELSOLTH 1554

Qy 421 GVTOLGFYVLDROSLFING 439
    |||
Db 1555 GVTOLGFYVLDROSLFING 1573

RESULT 4
US-11-066-316A-963
; Sequence 963, Application US/11066316A
; Publication No. US20070059710A1
; GENERAL INFORMATION:
; APPLICANT: Luke, May
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH STROKE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01585
; CURRENT APPLICATION NUMBER: US/11/066.316A
; CURRENT FILING DATE: 2005-02-25
; NUMBER OF SEQ ID NOS: 55503
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 963
; LENGTH: 13888
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-066-316A-963
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Query Match      99.8%; Score 2317; DB 7; Length 13888;
Best Local Similarity 99.8%; Pred. No. 1.2e-177;
Matches 438; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||
Db 13133 FTHRSSVSTSTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 13192

Qy 61 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 120
    |||
Db 13193 SRKFNTERVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 13252

Qy 121 GLDREQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||
Db 13253 GLDREQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 13312

Qy 181 INNLRYMADMGPQGSLSKENITDNVMQHLLSPLFQSSSLGARTGCRVIALRSVKNGAETR 240
    |||
Db 13313 INNLRYMADMGPQGSLSKENITDNVMQHLLSPLFQSSSLGARTGCRVIALRSVKNGAETR 13372

Qy 241 VDLCTYLOPLSGPGLPIKQVFHELSSQOOTHGITRLGYPYSLDKDSLYLNGYNPEGPDEPPT 300
    |||
Db 13373 VDLCTYLOPLSGPGLPIKQVFHELSSQOOTHGITRLGYPYSLDKDSLYLNGYNPEGPDEPPT 13432

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMKSGSATFNSTEGVLQHLRL 360
    |||
Db 13433 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMKSGSATFNSTEGVLQHLRL 13492

Qy 361 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVTCTYHPDPVPGGLDIQOLYLWELSOLTH 420
    |||
Db 13493 PLFKSSMGPFYLGCOLISLRPEKDGAAATGVTCTYHPDPVPGGLDIQOLYLWELSOLTH 13552

Qy 421 GVTOLGFYVLDROSLFING 439
    |||
Db 13553 GVTOLGFYVLDROSLFING 13571

RESULT 5
US-11-443-428A-775223
; Sequence 775223, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCE
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 775223
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; LENGTH: 1890
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-443-428A-775223

Query Match          99.6%; Score 2311; DB 7; Length 1890;
Best Local Similarity 99.8%; Pred. No. 2.7e-178;
Matches 438; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||||||
Db 1135 FTHRSSVSTTSGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 1194

Qy 61 SRKFNTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLRPEKDGATGVDAICTHRPDPGTP 120
    |||||||
Db 1195 SRKFNTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLRPEKDGATGVDAICTHRPDPGTP 1254

Qy 121 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSGVVSEEPFTLNFT 180
    |||||||
Db 1255 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSGVVSEEPFTLNFT 1314

Qy 181 INNLRYADMGGPGSLKFNITDNWKKHLLSPLFQSSSLGARVTGCRVIALRSVKNGAETR 240
    |||||||
Db 1315 INNLRYADMGGPGSLKFNITDNWKKHLLSPLFQSSSLGARVTGCRVIALRSVKNGAETR 1374

Qy 241 VDLICTYLOPLSGGGLPIKQVFHELSSQOOTHGITRLGPGYSLDKDSLXYNGYNPGDEPPT 300
    |||||||
Db 1375 VDLICTYLOPLSGGGLPIKQVFHELSSQOOTHGITRLGPGYSLDKDSLXYNGYNPGDEPPT 1434

Qy 301 TPKPATTFPLPSEATTANGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
    |||||||
Db 1435 TPKPATTFPLPSEATTANGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 1494

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 420
    |||||||
Db 1495 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 1554

Qy 421 GVTOLGFFYVLDRLDSLFG 439
    |||||||
Db 1555 GVTOLGFFYVLDRLDSLFG 1573

RESULT 6
US-10-475-117-48
; Sequence 48, Application US/10475117
; Publication No. US20070015907A1
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Arkansas
; APPLICANT: O'Brien, Timothy
; APPLICANT: Beard, John
; APPLICANT: Underwood, Lowell
; TITLE OF INVENTION: CA125 Gene and its Use for Diagnostic and Therapeutic
; TITLE OF INVENTION: Interventions
; FILE REFERENCE: 022438.43867
; CURRENT APPLICATION NUMBER: US/10/475.117
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/US02/11734
; PRIOR FILING DATE: 2002-04-12
; PRIOR APPLICATION NUMBER: 60/284,175
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/299,380
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; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 09/965,738
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/427,045
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: 60/345,180
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 48
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-475-117-48

Query Match          99.1%; Score 2301; DB 6; Length 1148;
Best Local Similarity 99.5%; Pred. No. 9.3e-178;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |||||||
Db 393 FTHRSSVSTTSGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 452

Qy 61 SRKFNTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLRPEKDGATGVDAICTHRPDPGTP 120
    |||||||
Db 453 SRKFNTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLRPEKDGATGVDAICTHRPDPGTP 512

Qy 121 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSGVVSEEPFTLNFT 180
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Db 513 GLDREQLYLELSQTHSITELGPTTLDRLSLYVNGFTHRSSVPTTSGVVSEEPFTLNFT 572

Qy 181 INNLRYADMGGPGSLKFNITDNWKKHLLSPLFQSSSLGARVTGCRVIALRSVKNGAETR 240
    |||||||
Db 573 INNLRYADMGGPGSLKFNITDNWKKHLLSPLFQSSSLGARVTGCRVIALRSVKNGAETR 632

Qy 241 VDLICTYLOPLSGGGLPIKQVFHELSSQOOTHGITRLGPGYSLDKDSLXYNGYNPGDEPPT 300
    |||||||
Db 633 VDLICTYLOPLSGGGLPIKQVFHELSSQOOTHGITRLGPGYSLDKDSLXYNGYNPGDEPPT 692

Qy 301 TPKPATTFPLPSEATTANGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
    |||||||
Db 693 TPKPATTFPLPSEATTANGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 752

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 420
    |||||||
Db 753 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 812

Qy 421 GVTOLGFFYVLDRLDSLFG 439
    |||||||
Db 813 GVTOLGFFYVLDRLDSLFG 831

RESULT 7
US-10-917-503-18865
; Sequence 18865, Application US/10917503
; Publication No. US20070105122A1
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
```

APPLICANT: SAITO, KAORU
APPLICANT: YAMAMOTO, JUNICHI
APPLICANT: ISHII, SHIZUKO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: NAKAMATSU, AI
APPLICANT: NAGAI, KEIICHI
APPLICANT: OTSUKI, TETSUJI
TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
FILE REFERENCE: 084335/0123
CURRENT APPLICATION NUMBER: US/10/917,503
CURRENT FILING DATE: 2004-08-13
PRIOR APPLICATION NUMBER: US/09/629,469
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: JP 1999-248036
PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: JP 1999-300253
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: JP 2000-118776
PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 2000-241899
PRIOR FILING DATE: 2000-06-09
PRIOR APPLICATION NUMBER: 60/159,590
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: 60/183,322
PRIOR FILING DATE: 2000-02-17
NUMBER OF SEQ ID NOS: 19025
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18865
LENGTH: 1148
TYPE: PRT
ORGANISM: Homo sapiens
US-10-917-503-18865

Query Match 99.1%; Score 2301; DB 6; Length 1148;
Best Local Similarity 99.5%; Pred. No. 9.3e-178;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSPGTPVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
|||||
Db 393 FTHRSSVSTTSPGTPVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 452

Qy 61 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPTGP 120
|||||
Db 453 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGSRLLTLRPEKDGATGDAICTHRPDPTGP 512

Qy 121 GLDREQLYLELSOLTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
|||||
Db 513 GLDREQLYLELSOLTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 572

Qy 181 INNLRYWADMGQPGSLKFNITDNVVKHLLSPLFORSSILGARYTCRCVIALRSVKNGAETR 240
|||||
Db 573 INNLRYWADMGQPGSLKFNITDNVVKHLLSPLFORSSILGARYTCRCVIALRSVKNGAETR 632

Qy 241 VOLLCYTLQPLSGPLPIKQVFHELSSQOOTHGIFRLGPLYSLDKDSLYNGYNEPGDPPT 300
|||||
Db 633 VOLLCYTLQPLSGPLPIKQVFHELSSQOOTHGIFRLGPLYSLDKDSLYNGYNEPGDPPT 692

Qy 301 TKPATTFPLPSEATTAGYHLKTLTNFTISNLQYSPDMKGKSATFNSTEGVLQHLR 360
|||||

Db 693 TPKPATTFPLPSEATTAGYHLKTLTNFTISNLQYSPDMKGKSATFNSTEGVLQHLR 752

Qy 361 PLFKSSNGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQOLYWELSOLTH 420
|||||
Db 753 PLFKSSNGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQOLYWELSOLTH 812

Qy 421 GVTOLGFVLDRLDSLFING 439
|||||
Db 813 GVTOLGFVLDRLDSLFING 831

RESULT 8
US-11-105-233-195
Sequence 195, Application US/11105233
Publication No. US20060134653A1
GENERAL INFORMATION:
APPLICANT: Thiagalingam et al
TITLE OF INVENTION: Differential Expression of Genes in MSI
TITLE OF INVENTION: Tumors
FILE REFERENCE: 1657/2001
CURRENT APPLICATION NUMBER: US/11/105,233
CURRENT FILING DATE: 2005-04-13
NUMBER OF SEQ ID NOS: 202
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 195
LENGTH: 1148
TYPE: PRT
ORGANISM: Homo sapiens
US-11-105-233-195

Query Match 99.1%; Score 2301; DB 7; Length 1148;
Best Local Similarity 99.5%; Pred. No. 9.3e-178;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSPGTPVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
|||||
Db 393 FTHRSSVSTTSPGTPVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 452

Qy 61 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGDAICTHRPDPTGP 120
|||||
Db 453 SRKNTTTERVLOGLLRPLFKNTSVGPLYSGSRLLTLRPEKDGATGDAICTHRPDPTGP 512

Qy 121 GLDREQLYLELSOLTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
|||||
Db 513 GLDREQLYLELSOLTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 572

Qy 181 INNLRYWADMGQPGSLKFNITDNVVKHLLSPLFORSSILGARYTCRCVIALRSVKNGAETR 240
|||||
Db 573 INNLRYWADMGQPGSLKFNITDNVVKHLLSPLFORSSILGARYTCRCVIALRSVKNGAETR 632

Qy 241 VOLLCYTLQPLSGPLPIKQVFHELSSQOOTHGIFRLGPLYSLDKDSLYNGYNEPGDPPT 300
|||||
Db 633 VOLLCYTLQPLSGPLPIKQVFHELSSQOOTHGIFRLGPLYSLDKDSLYNGYNEPGDPPT 692

Qy 301 TPKPATTFPLPSEATTAGYHLKTLTNFTISNLQYSPDMKGKSATFNSTEGVLQHLR 360
|||||
Db 693 TPKPATTFPLPSEATTAGYHLKTLTNFTISNLQYSPDMKGKSATFNSTEGVLQHLR 752

Qy 361 PLFKSSNGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQOLYWELSOLTH 420
|||||
Db 753 PLFKSSNGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQOLYWELSOLTH 812


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Qy      421  GVTGLGYVLDROSLFNG 439
          | | | | | | | | | | | | | | | |
Db      813  GVTGLGYVLDROSLFNG 831

RESULT 9
US-11-226-554-129
; Sequence 129, Application US/11226554
; Publication No. US20060147373A1
; GENERAL INFORMATION:
; APPLICANT: Cairns,Belinda
; APPLICANT: Chen,Ruihan
; APPLICANT: Franz,Gretchen
; APPLICANT: Hillan,Kenneth J.
; APPLICANT: Koepfen,Hartmut
; APPLICANT: Phillips,Heidi S.
; APPLICANT: Polakis,Paul
; APPLICANT: Spencer,Susan D.
; APPLICANT: Smith,Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu,Thomas D.
; APPLICANT: Zhang,Zemin
; TITLE OF INVENTION: Compositions and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1C1
; CURRENT APPLICATION NUMBER: US/11/226
; CURRENT FILING DATE: 2005-09-13
; PRIOR APPLICATION NUMBER: US 10/177,
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/366,
; PRIOR FILING DATE: 2002-03-20
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 129
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-226-554-129

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Query Match	99.1%;	Score 2301;	DB 7;	Length 1148;
Best local Similarity	99.5%;	Pred. No. 9.3e-178;		
Matches 437;	Conservative 0;	Mismatches 172;	Indels 0;	Gaps 0;
Qy	1	FTHRSSVSTTPTGTTTIVYLGASKTPTASIFGSPASASHLLILFTLNTFTINLRYEENWPG	60	
Db	393	FTHRSSVSTTPTGTTTIVYLGASKTPTASIFGSPASASHLLILFTLNTFTINLRYEENWPG	452	
Qy	61	SRKENTTERRVLOGLLRPLFKNTSVGPLYSGGRLLTLRLPEKDEATGVDAICTHRPDPDTP	120	
Db	453	SRKENTTERRVLOGLLRPLFKNTSVGPLYSGGRLLTLRLPEKDEATGVDAICTHRPDPDTP	512	
Qy	121	GLDREQLYLELSQLTISITELGPTYTLDRDSLTVYNGFTHRSSVPTTSTGVVSEEPFTLNT	180	
Db	513	GLDREQLYLELSQLTISITELGPTYTLDRDSLTVYNGFTHRSSVPTTSTGVVSEEPFTLNT	572	
Qy	181	INNLRYMADMQPGSKLKFNIITDMVAKHLLSPFORSSLGARVTGCRVIALRSVKNGAETR	240	
Db	573	INNLRYMADMQPGSKLKFNIITDMVAKHLLSPFORSSLGARVTGCRVIALRSVKNGAETR	632	
Qy	241	VOLLCTYLPQLSGPGIPIKOVFHELSSQTHGICTRLGPFYSLDKDSLTVINGYNEPGPDEPT	300	

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Db      633  VOLLCITYQLPSGPGKIQVHFELSSQOHTIGITRUGPYSLDKDSLYILNGNEPGLDEPPT 692
Qy      301  TPKPATTFLPPLSEATTAMGYHLKLTTLNFTISNLOQSPDMGKSATFNSTEGVLOHLR 360
        |||||||
Db      693  TPKPATTFLPPLSEATTAMGYHLKLTTLNFTISNLOQSPDMGKSATFNSTEGVLOHLR 752
Qy      361  PLFQKSMGPFYLGCOLLSLRPEKDGAAATGVDTCTYHPDPVPGGLDIQOLYWELSQLT 420
        |||||||
Db      753  PLFQKSMGPFYLGCOLLSLRPEKDGAAATGVDTCTYHPDPVPGGLDIQOLYWELSQLT 812
Qy      421  GVTQLGFEVLDROSLFNG 439
        |||||||
Db      813  GVTQLGFEVLDROSLFNG 831

RESULT 10
US-11-248-718-129
; Sequence 129, Application US/11248718
; Publication No. US20060160997A1
; GENERAL INFORMATION:
; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koeppen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1 US
; CURRENT APPLICATION NUMBER: US/11/248,718
; CURRENT FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/300,880
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/304,813
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/312,312
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 60/314,280
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/339,227
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/336,827
; PRIOR FILING DATE: 2001-11-07
; Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 129
; LENGTH: 1148

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; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-248-718-129

Query Match          99.1%; Score 2301; DB 7; Length 1148;
Best Local Similarity 99.5%; Pred. No. 9.3e-178;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTHRSSVSTSTGCTPTVVLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
    |||||||
Db 393 FTHRSSVSTSTGCTPTVVLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 452

QY 61 SRKENTTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
    |||||||
Db 453 SRKENTTTERVLOGLLRPLFKNTSVGPLYSGSRLLTLRPEKDGATGVDAICTHRPDPTGP 512

QY 121 GLDREQLYLELSQUTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||||||
Db 513 GLDREQLYLELSQUTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 572

QY 181 INNLRYMADMGOPGSLKFNITDNVWKHLLSPFORSSLGARTGCRVIALRSVKNGAETR 240
    |||||||
Db 573 INNLRYMADMGOPGSLKFNITDNVWKHLLSPFORSSLGARTGCRVIALRSVKNGAETR 632

QY 241 VDLCTYLIQPLSGPLPIKOVFHELSQOOTHGITRLGYPYSLDKDSLYLNGYNEPGDPPT 300
    |||||||
Db 633 VDLCTYLIQPLSGPLPIKOVFHELSQOOTHGITRLGYPYSLDKDSLYLNGYNEPGDPPT 692

QY 301 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTGVLOHLR 360
    |||||||
Db 693 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTGVLOHLR 752

QY 361 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 420
    |||||||
Db 753 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 812

QY 421 GVTOLGFYVLDSDSLFING 439
    |||||||
Db 813 GVTOLGFYVLDSDSLFING 831

RESULT 11
US-11-538-552-129
; Sequence 129, Application US/11538552
; Publication No. US20070048326A1
; GENERAL INFORMATION:
; APPLICANT: Cairns, Belinda
; APPLICANT: Chen, Ruihuan
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Koepfen, Hartmut
; APPLICANT: Phillips, Heidi S.
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan D.
; APPLICANT: Smith, Victoria
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas D.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumor
; FILE REFERENCE: P5001R1 US
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; CURRENT APPLICATION NUMBER: US/11/538,552
; CURRENT FILING DATE: 2006-10-04
; PRIOR APPLICATION NUMBER: US/11/248,718
; PRIOR FILING DATE: 2005-10-11
; PRIOR APPLICATION NUMBER: US/10/177,488
; PRIOR FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US 60/299,500
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: US 60/300,880
; PRIOR FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/301,880
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/304,813
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: US 60/312,312
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 60/314,280
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 60/339,227
; PRIOR FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: US 60/323,268
; PRIOR FILING DATE: 2001-09-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 154
; SEQ ID NO 129
; LENGTH: 1148
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-538-552-129

Query Match          99.1%; Score 2301; DB 7; Length 1148;
Best Local Similarity 99.5%; Pred. No. 9.3e-178;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 FTHRSSVSTSTGCTPTVVLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
    |||||||
Db 393 FTHRSSVSTSTGCTPTVVLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 452

QY 61 SRKENTTTERVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
    |||||||
Db 453 SRKENTTTERVLOGLLRPLFKNTSVGPLYSGSRLLTLRPEKDGATGVDAICTHRPDPTGP 512

QY 121 GLDREQLYLELSQUTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |||||||
Db 513 GLDREQLYLELSQUTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 572

QY 181 INNLRYMADMGOPGSLKFNITDNVWKHLLSPFORSSLGARTGCRVIALRSVKNGAETR 240
    |||||||
Db 573 INNLRYMADMGOPGSLKFNITDNVWKHLLSPFORSSLGARTGCRVIALRSVKNGAETR 632

QY 241 VDLCTYLIQPLSGPLPIKOVFHELSQOOTHGITRLGYPYSLDKDSLYLNGYNEPGDPPT 300
    |||||||
Db 633 VDLCTYLIQPLSGPLPIKOVFHELSQOOTHGITRLGYPYSLDKDSLYLNGYNEPGDPPT 692

QY 301 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTGVLOHLR 360
    |||||||
Db 693 TPKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTGVLOHLR 752

QY 361 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 420
    |||||||
Db 753 PLFQKSSMGPFYLGCOLISLRPEKGAATGVDTTCTYHPDPVPGGLDIQOLYWELSQLTH 812
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Qy 61 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
      |||
Db 9388 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGSRLLTLRPEKDGATGVDAICTHRPDPTGP 9447
      |||
Qy 121 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
      |||
Db 9448 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 9507
      |||
Qy 181 INNLRYMADMGQPGSLKFNITDNVMKHLSPLFQRSSLGARYTGCRIALRSVKNGAETR 240
      |||
Db 9508 INNLRYMADMGQPGSLKFNITDNVMKHLSPLFQRSSLGARYTGCRIALRSVKNGAETR 9567
      |||
Qy 241 VDLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPLYSLDKDSLYLNGYNEPGDEPPT 300
      |||
Db 9568 VDLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPLYSLDKDSLYLNGYNEPGDEPPT 9627
      |||
Qy 301 TKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 360
      |||
Db 9628 TKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 9687
      |||
Qy 361 PLFOKSSMGPFYLGCOLLSLRPEKDGATGVDTTCTYHPDPVGPGLDIOQLYWELSOLTH 420
      |||
Db 9688 PLFOKSSMGPFYLGCOLLSLRPEKDGATGVDTTCTYHPDPVGPGLDIOQLYWELSOLTH 9747
      |||
Qy 421 GVTOLGFYVLDROSLFNG 439
      |||
Db 9748 GVTOLGFYVLDROSLFNG 9766
      |||
```

```
RESULT 14
US-10-475-117-162
; Sequence 162, Application US/10475117
; Publication No. US20070015907A1
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Arkansas
; APPLICANT: O'Brien, Timothy
; APPLICANT: Beard, John
; APPLICANT: Underwood, Lowell
; TITLE OF INVENTION: CA125 Gene and its Use for Diagnostic and Therapeutic
; FILE REFERENCE: 022438.43867
; CURRENT APPLICATION NUMBER: US/10/475.117
; PRIOR FILING DATE: 2003-10-17
; PRIOR FILING DATE: PCT/US02/11734
; PRIOR FILING DATE: 2002-04-12
; PRIOR FILING DATE: 60/284,175
; PRIOR FILING DATE: 2001-04-17
; PRIOR FILING DATE: 60/299,380
; PRIOR FILING DATE: 2001-06-19
; PRIOR FILING DATE: 09/965,738
; PRIOR FILING DATE: 2001-09-27
; PRIOR FILING DATE: 60/427,045
; PRIOR FILING DATE: 2002-11-15
; PRIOR FILING DATE: 60/345,180
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 162
; LENGTH: 11721
; TYPE: PRT
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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(11721)
; OTHER INFORMATION: Any "X" = any amino acid
US-10-475-117-162

Query Match 99.1%; Score 2301; DB 6; Length 11721;
Best Local Similarity 99.5%; Pred. No. 1.9e-176;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTTVYLGASKTPASIFGSAASHLLILFTLNFTINLRVEENWPG 60
      |||
Db 10966 FTHRSSVSTTSGTPTTVYLGASKTPASIFGSAASHLLILFTLNFTINLRVEENWPG 11025
      |||
Qy 61 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
      |||
Db 11026 SRKNTTERTVLOGLLRPLFKNTSVGPLYSGSRLLTLRPEKDGATGVDAICTHRPDPTGP 11085
      |||
Qy 121 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
      |||
Db 11086 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 11145
      |||
Qy 181 INNLRYMADMGQPGSLKFNITDNVMKHLSPLFQRSSLGARYTGCRIALRSVKNGAETR 240
      |||
Db 11146 INNLRYMADMGQPGSLKFNITDNVMKHLSPLFQRSSLGARYTGCRIALRSVKNGAETR 11205
      |||
Qy 241 VDLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPLYSLDKDSLYLNGYNEPGDEPPT 300
      |||
Db 11206 VDLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPLYSLDKDSLYLNGYNEPGDEPPT 11265
      |||
Qy 301 TKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 360
      |||
Db 11266 TKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLOHLLR 11325
      |||
Qy 361 PLFOKSSMGPFYLGCOLLSLRPEKDGATGVDTTCTYHPDPVGPGLDIOQLYWELSOLTH 420
      |||
Db 11326 PLFOKSSMGPFYLGCOLLSLRPEKDGATGVDTTCTYHPDPVGPGLDIOQLYWELSOLTH 11385
      |||
Qy 421 GVTOLGFYVLDROSLFNG 439
      |||
Db 11386 GVTOLGFYVLDROSLFNG 11404
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RESULT 15
US-10-544-944-1
; Sequence 1, Application US/10544944
; Publication No. US20060134120A1
; GENERAL INFORMATION:
; APPLICANT: Diamandis, Eleftherios P.
; TITLE OF INVENTION: Multiple Marker Assay for Detection of Ovarian Cancer
; FILE REFERENCE: 11757.0088USMO
; CURRENT APPLICATION NUMBER: US/10/544,944
; CURRENT FILING DATE: 2005-08-09
; PRIOR APPLICATION NUMBER: PCT/CA2004/000281
; PRIOR FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US 60/450,406
; PRIOR FILING DATE: 2003-02-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
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; LENGTH: 22152
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13877)..(13878)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13880)..(13880)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13887)..(13887)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13890)..(13891)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13893)..(13893)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13903)..(13903)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13913)..(13914)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13916)..(13916)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13928)..(13929)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13938)..(13938)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13940)..(13941)
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Best Local Similarity 99.5%; Pred. No. 4.4e-176;
Matches 437; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 21397 FTHRSSVSTTSTPGTPVYLGASKTPASIFCPASAASHLLILFLTNFTITNLRYEENWPG 21456
Qy 61 SRKNTTTERVLOGLLRPLFKNTSVGLYSGCRUTLLRPEKDGATGVDAICTHRPDTGP 120
Db 21457 SRKNTTTERVLOGLLRPLFKNTSVGLYSGSRUTLLRPEKDGATGVDAICTHRPDTGP 21516
Qy 121 GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 21517 GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 21576
Qy 181 INNLRYMADMGQPSLKENITDNVMKLLSPLFORSSLGARYTCRVIALRSVKNGAETR 240
Db 21577 INNLRYMADMGQPSLKENITDNVMKLLSPLFORSSLGARYTCRVIALRSVKNGAETR 21636
Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGYSLOKDSLTVNGYNEPGPDEPPT 300
Db 21637 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGYSLOKDSLTVNGYNEPGPDEPPT 21696
Qy 301 TKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
Db 21697 TKPATTFLPPLSEATTAMGYHLKTLTNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 21756
Qy 361 PLFOKSSMGFFYLGQLISLRPEKDGATGVDTTCTYHHPDPVGPGLDIQOLYWELSQLTH 420
Db 21757 PLFOKSSMGFFYLGQLISLRPEKDGATGVDTTCTYHHPDPVGPGLDIQOLYWELSQLTH 21816
Qy 421 GVTQLGFVLDRLSLFING 439
Db 21817 GVTQLGFVLDRLSLFING 21835

Search completed: June 7, 2007, 18:03:08
Job time : 314 secs

SCORE 2.0 BuildDate: 12/03/2005

SCORE Search Results Details for Application
10687035 and Search Result
20070607_154745_us-10-687-035-
1_copy_14_452.rapbm.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10687035 and Search Result 20070607_154745_us-10-687-035-1_copy_14_452.rapbm.

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OM protein - protein search, using sw model

Run on: June 7, 2007, 17:53:46 ; Search time 188 Seconds
(without alignments)
1081.656 Million cell updates/sec

Title: US-10-687-035-1_COPY_14_452

Sequence: 1 FTHRSSVSTTSGPTVYL.....HGVTLGFGYLDRLSLFNG 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
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- 6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Query Match	Length	DB	ID	Description
1	2321	100.0	748	5	US-10-687-035-1	Sequence 1, Appli
2	2321	100.0	772	3	US-09-884-441-388	Sequence 388, App
3	2321	100.0	772	3	US-09-907-969-388	Sequence 388, App
4	2321	100.0	772	3	US-09-827-271-388	Sequence 388, App
5	2321	100.0	772	4	US-10-198-053-388	Sequence 388, App
6	2321	100.0	772	5	US-10-860-790-388	Sequence 388, App
7	2321	100.0	809	5	US-10-687-035-2	Sequence 2, Appli
8	2321	100.0	833	3	US-09-884-441-389	Sequence 389, App
9	2321	100.0	833	3	US-09-907-969-389	Sequence 389, App
10	2321	100.0	833	3	US-09-827-271-389	Sequence 389, App
11	2321	100.0	833	4	US-10-198-053-389	Sequence 389, App
12	2321	100.0	833	5	US-10-860-790-389	Sequence 389, App
13	2321	100.0	914	3	US-09-778-320-206	Sequence 206, App
14	2321	100.0	914	3	US-09-910-689-206	Sequence 206, App
15	2321	100.0	914	3	US-09-884-441-312	Sequence 312, App
16	2321	100.0	914	3	US-09-884-441-478	Sequence 478, App
17	2321	100.0	914	3	US-09-907-969-312	Sequence 312, App
18	2321	100.0	914	3	US-09-907-969-478	Sequence 478, App
19	2321	100.0	914	3	US-09-827-271-312	Sequence 312, App
20	2321	100.0	914	4	US-10-010-742-206	Sequence 206, App
21	2321	100.0	914	4	US-10-198-053-312	Sequence 312, App
22	2321	100.0	914	4	US-10-198-053-478	Sequence 478, App
23	2321	100.0	914	4	US-10-714-389-206	Sequence 206, App
24	2321	100.0	914	4	US-10-717-296-206	Sequence 206, App
25	2321	100.0	914	5	US-10-860-790-312	Sequence 312, App
26	2321	100.0	914	5	US-10-860-790-478	Sequence 478, App
27	2317	99.8	1889	4	US-10-142-515-5	Sequence 5, Appli
28	2317	99.8	1890	4	US-10-097-340-217	Sequence 217, App
29	2317	99.8	1890	4	US-10-245-871-314	Sequence 314, App
30	2317	99.8	1890	4	US-10-253-286-314	Sequence 314, App
31	2317	99.8	1890	6	US-11-050-926-217	Sequence 217, App
32	2317	99.8	1890	6	US-11-033-039-314	Sequence 314, App
33	2317	99.8	6995	5	US-10-983-360-4	Sequence 4, Appli
34	2312	99.6	3451	3	US-09-907-969-595	Sequence 595, App
35	2312	99.6	3451	4	US-10-198-053-595	Sequence 595, App
36	2312	99.6	3451	5	US-10-860-790-595	Sequence 595, App
37	2301	99.1	1148	3	US-09-884-441-458	Sequence 458, App
38	2301	99.1	1148	3	US-09-884-441-479	Sequence 479, App
39	2301	99.1	1148	3	US-09-907-969-458	Sequence 458, App
40	2301	99.1	1148	3	US-09-907-969-479	Sequence 479, App
41	2301	99.1	1148	3	US-09-965-738-48	Sequence 48, Appl
42	2301	99.1	1148	3	US-09-827-271-458	Sequence 458, App
43	2301	99.1	1148	4	US-10-097-340-216	Sequence 216, App
44	2301	99.1	1148	4	US-10-198-053-458	Sequence 458, App
45	2301	99.1	1148	4	US-10-198-053-479	Sequence 479, App

ALIGNMENTS

RESULT 1
US-10-687-035-1
; Sequence 1, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albione, Earl F.
; APPLICANT: Solitis, Daniel A.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED

; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF
; FILE REFERENCE: 6750-214-999
; CURRENT APPLICATION NUMBER: US/10/687,035
; PRIOR FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 60/418,828
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 748
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CA 125/0772P 3-repeat
US-10-687-035-1

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Best Local Similarity 100.0%; Pred. No. 2e-200;
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Qy 1 FTHRSSVSTTPTGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60
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Db 14 FTHRSSVSTTPTGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 73

Qy 61 SRKENTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRLPEKDGATGVDAICTHRPDPTGP 120
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Db 74 SRKENTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRLPEKDGATGVDAICTHRPDPTGP 133

Qy 121 GLDREQLYLELSOLTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
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Db 134 GLDREQLYLELSOLTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193

Qy 181 INNLRYADMGPQSGSLKFNITDNVKKHLLSPLEFRSSILGARYTGCRIALRSVKNGAETR 240
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Db 194 INNLRYADMGPQSGSLKFNITDNVKKHLLSPLEFRSSILGARYTGCRIALRSVKNGAETR 253

Qy 241 VDLCTYLOPLSGPGLPIKOVFHELSQOOTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT 300
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Db 254 VDLCTYLOPLSGPGLPIKOVFHELSQOOTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT 313

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLQHLRL 360
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Db 314 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLQHLRL 373

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQOLYWELSOLTH 420
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Db 374 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQOLYWELSOLTH 433

Qy 421 GVTQLGFYVLDRLDSLIFNG 439
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Db 434 GVTQLGFYVLDRLDSLIFNG 452

RESULT 2
US-09-884-441-388
; Sequence 388, Application US/09884411
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.

; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-388

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Best Local Similarity 100.0%; Pred. No. 2.1e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTPTGPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60
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Db 219 SRKENTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRLPEKDGATGVDAICTHRPDPTGP 278

Qy 121 GLDREQLYLELSOLTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
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Db 279 GLDREQLYLELSOLTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338

Qy 181 INNLRYADMGPQSGSLKFNITDNVKKHLLSPLEFRSSILGARYTGCRIALRSVKNGAETR 240
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Db 339 INNLRYADMGPQSGSLKFNITDNVKKHLLSPLEFRSSILGARYTGCRIALRSVKNGAETR 398

Qy 241 VDLCTYLOPLSGPGLPIKOVFHELSQOOTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT 300
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Db 399 VDLCTYLOPLSGPGLPIKOVFHELSQOOTHGITRLGPYSLDKDSLYLNGYNEPGDEPPT 458

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLQHLRL 360
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Db 459 TPKPATTFLPPLSEATTAMGYHLKTLTLNFTISNLQVSPDMGKGSATFNSTEGVLQHLRL 518

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQOLYWELSOLTH 420
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Db 519 PLFOKSSMGPFYLGCOLISLRPEKDGATGVDTTCTYHPDPVGPGLDIQOLYWELSOLTH 578

Qy 421 GVTQLGFYVLDRLDSLIFNG 439
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Db 579 GVTQLGFYVLDRLDSLIFNG 597

RESULT 3
US-09-907-969-388
; Sequence 388, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.

; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Hill, Paul
; APPLICANT: Albone, Earl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-969-388

Query Match 100.0%; Score 2321; DB 3; Length 772;
Best Local Similarity 100.0%; Pred. No. 2.le-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTPTGTPPVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60
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DB 159 FTHRSSVSTTPTGTPPVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218
|||||

QY 61 SRKENTTERRVLOGLLRPLFKNTSGPLYSGCRLLTLRPEKDGATGDAICTHRPDTGP 120
|||||
DB 219 SRKENTTERRVLOGLLRPLFKNTSGPLYSGCRLLTLRPEKDGATGDAICTHRPDTGP 278
|||||

QY 121 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 180
|||||
DB 279 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 338
|||||

QY 181 INNLRYMADMGOPGSLKFENITDNVKKHLLSPLEFORSSLGARYTGCRRVIALRSVKNGAETR 240
|||||
DB 339 INNLRYMADMGOPGSLKFENITDNVKKHLLSPLEFORSSLGARYTGCRRVIALRSVKNGAETR 398
|||||

QY 241 VDLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 300
|||||
DB 399 VDLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 458
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QY 301 TPKPATTFLPPLSEATTAKGYHLKTLTNFTISNLOYSPDMGKGSATFNSTEGVLOHLLR 360
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DB 459 TPKPATTFLPPLSEATTAKGYHLKTLTNFTISNLOYSPDMGKGSATFNSTEGVLOHLLR 518
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QY 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVTCTTCTYHPDPVPGGLDIQOLYWELSOLTH 420
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DB 519 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVTCTTCTYHPDPVPGGLDIQOLYWELSOLTH 578
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QY 421 GVTOLGFYVLDNRDSLIFNG 439
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DB 579 GVTOLGFYVLDNRDSLIFNG 597
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RESULT 4
US-09-827-271-388
; Sequence 388, Application US/09827271
; Publication No. US2003016504A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul

; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-388

Query Match 100.0%; Score 2321; DB 3; Length 772;
Best Local Similarity 100.0%; Pred. No. 2.le-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTPTGTPPVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60
|||||
DB 159 FTHRSSVSTTPTGTPPVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218
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QY 61 SRKENTTERRVLOGLLRPLFKNTSGPLYSGCRLLTLRPEKDGATGDAICTHRPDTGP 120
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DB 219 SRKENTTERRVLOGLLRPLFKNTSGPLYSGCRLLTLRPEKDGATGDAICTHRPDTGP 278
|||||

QY 121 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 180
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DB 279 GLDREQLYLELSQTHSITELGPYTLDRDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 338
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QY 181 INNLRYMADMGOPGSLKFENITDNVKKHLLSPLEFORSSLGARYTGCRRVIALRSVKNGAETR 240
|||||
DB 339 INNLRYMADMGOPGSLKFENITDNVKKHLLSPLEFORSSLGARYTGCRRVIALRSVKNGAETR 398
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QY 241 VDLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 300
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DB 399 VDLCTYLOPLSGPLPIKOVFHELSQOOTHGITRLGPGYSLDKDSLYLNGYNEPGDEPPT 458
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QY 301 TPKPATTFLPPLSEATTAKGYHLKTLTNFTISNLOYSPDMGKGSATFNSTEGVLOHLLR 360
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DB 459 TPKPATTFLPPLSEATTAKGYHLKTLTNFTISNLOYSPDMGKGSATFNSTEGVLOHLLR 518
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QY 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVTCTTCTYHPDPVPGGLDIQOLYWELSOLTH 420
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DB 519 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVTCTTCTYHPDPVPGGLDIQOLYWELSOLTH 578
|||||

QY 421 GVTOLGFYVLDNRDSLIFNG 439
|||||
DB 579 GVTOLGFYVLDNRDSLIFNG 597
|||||

RESULT 5
US-10-198-053-388
; Sequence 388, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul

```
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-388

Query Match      100.0%; Score 2321; DB 4; Length 772;
Best Local Similarity 100.0%; Pred. No. 2.1e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
Qy 61 SRKFNTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 120
Db 219 SRKFNTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 278
Qy 121 GLDREQLYLELSQTHSITELGPTVTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITELGPTVTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 181 INNLRYMADMGQPSLKNITDVMKHLSPFORSSLGARYTCGRVIALRSVKNGAETR 240
Db 339 INNLRYMADMGQPSLKNITDVMKHLSPFORSSLGARYTCGRVIALRSVKNGAETR 398
Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGPIYSLDKDSLYLVNGNEPGDEPPT 300
Db 399 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGPIYSLDKDSLYLVNGNEPGDEPPT 458
Qy 301 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
Db 459 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 518
Qy 361 PLFOKSSKGPFIYLGCOLISLRPEKDGATGVDTCTYHPDPVPGGLDIQQLYWELSQLTH 420
Db 519 PLFOKSSKGPFIYLGCOLISLRPEKDGATGVDTCTYHPDPVPGGLDIQQLYWELSQLTH 578
Qy 421 GVTQLGFYVLDRLDSLFING 439
Db 579 GVTQLGFYVLDRLDSLFING 597

RESULT 6
US-10-860-790-388
; Sequence 388, Application US/10860790
; Publication No. US20050031634A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
```

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; FILE REFERENCE: 210121.462C11
; CURRENT APPLICATION NUMBER: US/10/860,790
; CURRENT FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 388
; LENGTH: 772
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-860-790-388

Query Match      100.0%; Score 2321; DB 5; Length 772;
Best Local Similarity 100.0%; Pred. No. 2.1e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
Db 159 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 218
Qy 61 SRKFNTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 120
Db 219 SRKFNTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKDGATGVDAICTHRPDPGTP 278
Qy 121 GLDREQLYLELSQTHSITELGPTVTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
Db 279 GLDREQLYLELSQTHSITELGPTVTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 338
Qy 181 INNLRYMADMGQPSLKNITDVMKHLSPFORSSLGARYTCGRVIALRSVKNGAETR 240
Db 339 INNLRYMADMGQPSLKNITDVMKHLSPFORSSLGARYTCGRVIALRSVKNGAETR 398
Qy 241 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGPIYSLDKDSLYLVNGNEPGDEPPT 300
Db 399 VDLCTYLOPLSGPLPIKQVFHELSSQTHGITRLGPIYSLDKDSLYLVNGNEPGDEPPT 458
Qy 301 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 360
Db 459 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMGKGSATFNSTEGVLQHLR 518
Qy 361 PLFOKSSKGPFIYLGCOLISLRPEKDGATGVDTCTYHPDPVPGGLDIQQLYWELSQLTH 420
Db 519 PLFOKSSKGPFIYLGCOLISLRPEKDGATGVDTCTYHPDPVPGGLDIQQLYWELSQLTH 578
Qy 421 GVTQLGFYVLDRLDSLFING 439
Db 579 GVTQLGFYVLDRLDSLFING 597

RESULT 7
US-10-687-035-2
; Sequence 2, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albone, Earl F.
; APPLICANT: Soltis, Daniel A.
; TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
; TITLE OF INVENTION: CA 125/0772P AND METHODS OF USE THEREOF
; FILE REFERENCE: 6750-214-999
; CURRENT APPLICATION NUMBER: US/10/687,035
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: 60/485,986
```

; PRIOR FILING DATE: 2003-07-10
; PRIOR APPLICATION NUMBER: 60/418,828
; PRIOR FILING DATE: 2003-10-12
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CA 125/0772P 3-repeat TM
US-10-687-035-2

Query Match 100.0%; Score 2321; DB 5; Length 809;
Best Local Similarity 100.0%; Pred. No. 2.3e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTPTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
|||||
DB 14 FTHRSSVSTTPTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 73
|||||
QY 61 SRKENTTERTVQLGLRLPFLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
|||||
DB 74 SRKENTTERTVQLGLRLPFLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 133
|||||
QY 121 GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
|||||
DB 134 GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 193
|||||
QY 181 INNLRYADMGPQSLKFNITDNVVKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR 240
|||||
DB 194 INNLRYADMGPQSLKFNITDNVVKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR 253
|||||
QY 241 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGITRLGPGYSLDKDSLVLNGYNRPGDEPPT 300
|||||
DB 254 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGITRLGPGYSLDKDSLVLNGYNRPGDEPPT 313
|||||
QY 301 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMKGSAFNSGVLQHLRL 360
|||||
DB 314 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMKGSAFNSGVLQHLRL 373
|||||
QY 361 PLFKSSMGPFFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 420
|||||
DB 374 PLFKSSMGPFFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 433
|||||
QY 421 GVTQLGFYVLDRLDSLFTNG 439
|||||
DB 434 GVTQLGFYVLDRLDSLFTNG 452
|||||

RESULT 8
US-09-884-441-389
; Sequence 389, Application US/0988441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441

; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-884-441-389

Query Match 100.0%; Score 2321; DB 3; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.4e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTHRSSVSTTPTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
|||||
DB 78 FTHRSSVSTTPTGCTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 137
|||||
QY 61 SRKENTTERTVQLGLRLPFLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 120
|||||
DB 138 SRKENTTERTVQLGLRLPFLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRPDPTGP 197
|||||
QY 121 GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
|||||
DB 198 GLDREQLYLELSQTHSITELGPYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257
|||||
QY 181 INNLRYADMGPQSLKFNITDNVVKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR 240
|||||
DB 258 INNLRYADMGPQSLKFNITDNVVKHLLSPLFQRSSLGARYTGCVRVIALRSVKNGAETR 317
|||||
QY 241 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGITRLGPGYSLDKDSLVLNGYNRPGDEPPT 300
|||||
DB 318 VDLCTYLOPLSGPGLPIKQVFHELSSQTHGITRLGPGYSLDKDSLVLNGYNRPGDEPPT 377
|||||
QY 301 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMKGSAFNSGVLQHLRL 360
|||||
DB 378 TPKPATTFLPPLSEATTANGYHLKTLTLNFTISNLQYSPDMKGSAFNSGVLQHLRL 437
|||||
QY 361 PLFKSSMGPFFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 420
|||||
DB 438 PLFKSSMGPFFYLGCOLISLRPEKDGATGVDTTCTYHPDPVPGGLDIQQLYWELSQLTH 497
|||||
QY 421 GVTQLGFYVLDRLDSLFTNG 439
|||||
DB 498 GVTQLGFYVLDRLDSLFTNG 516
|||||

RESULT 9
US-09-907-969-389
; Sequence 389, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Hill, Paul

```
; APPLICANT: Albone, Earl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSEQ for windows Version 4.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-969-389

Query Match      100.0%; Score 2321; DB 3; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.4e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
    |||||||
Db 78 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 137
    |||||||

Qy 61 SKKENTTERRVLOGLLRPLFKNTSVGLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 120
    |||||||
Db 138 SKKENTTERRVLOGLLRPLFKNTSVGLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 197
    |||||||

Qy 121 GLDREQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSGVWSEEPFTLNFT 180
    |||||||
Db 198 GLDREQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSGVWSEEPFTLNFT 257
    |||||||

Qy 181 INNLRYMADMGQPGSLKFNITDNVKKHLLSPLEFORSSILGARYTGCRVIALRSVKNGAETR 240
    |||||||
Db 258 INNLRYMADMGQPGSLKFNITDNVKKHLLSPLEFORSSILGARYTGCRVIALRSVKNGAETR 317
    |||||||

Qy 241 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPTSLDKDSLYLNGYNEPGDEPPT 300
    |||||||
Db 318 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPTSLDKDSLYLNGYNEPGDEPPT 377
    |||||||

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMKGSATNSTEGVLOHLRL 360
    |||||||
Db 378 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMKGSATNSTEGVLOHLRL 437
    |||||||

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
    |||||||
Db 438 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 497
    |||||||

Qy 421 GVTOLGFYVLDRLDSLIFNG 439
    |||||||
Db 498 GVTOLGFYVLDRLDSLIFNG 516

RESULT 10
US-09-827-271-389
; Sequence 389, Application US/09827271
; Publication No. US2003016504A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
```

```
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-389

Query Match      100.0%; Score 2321; DB 3; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.4e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 60
    |||||||
Db 78 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWPG 137
    |||||||

Qy 61 SKKENTTERRVLOGLLRPLFKNTSVGLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 120
    |||||||
Db 138 SKKENTTERRVLOGLLRPLFKNTSVGLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 197
    |||||||

Qy 121 GLDREQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSGVWSEEPFTLNFT 180
    |||||||
Db 198 GLDREQLYLELSQTHSITELGPTTLDROSLYVNGFTHRSSVPTTSGVWSEEPFTLNFT 257
    |||||||

Qy 181 INNLRYMADMGQPGSLKFNITDNVKKHLLSPLEFORSSILGARYTGCRVIALRSVKNGAETR 240
    |||||||
Db 258 INNLRYMADMGQPGSLKFNITDNVKKHLLSPLEFORSSILGARYTGCRVIALRSVKNGAETR 317
    |||||||

Qy 241 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPTSLDKDSLYLNGYNEPGDEPPT 300
    |||||||
Db 318 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPTSLDKDSLYLNGYNEPGDEPPT 377
    |||||||

Qy 301 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMKGSATNSTEGVLOHLRL 360
    |||||||
Db 378 TPKPATTFLPPLSEATTAMGYHLKTLTNFTISNLOYSPDMKGSATNSTEGVLOHLRL 437
    |||||||

Qy 361 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 420
    |||||||
Db 438 PLFOKSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTYHPDPVPGGLDIOQLYWELSQLTH 497
    |||||||

Qy 421 GVTOLGFYVLDRLDSLIFNG 439
    |||||||
Db 498 GVTOLGFYVLDRLDSLIFNG 516

RESULT 11
US-10-198-053-389
; Sequence 389, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
```

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; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-389

Query Match      100.0%; Score 2321; DB 4; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.4e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |
Db 78 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 137
    |
Qy 61 SRKFTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKOGAATGDAICTHRPDPGTP 120
    |
Db 138 SRKFTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKOGAATGDAICTHRPDPGTP 197
    |
Qy 121 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |
Db 198 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257
    |
Qy 181 INNLRYADMADQPGSLKFNITDNVWKHLSPFLFORSSLGARYTCRVIALRSVKNGAETR 240
    |
Db 258 INNLRYADMADQPGSLKFNITDNVWKHLSPFLFORSSLGARYTCRVIALRSVKNGAETR 317
    |
Qy 241 VDLCTYLOPLSGPGLPIKQVFEHLSQOHTGILTRGYPYSLDKDSLYLNGYNEPGDEPPT 300
    |
Db 318 VDLCTYLOPLSGPGLPIKQVFEHLSQOHTGILTRGYPYSLDKDSLYLNGYNEPGDEPPT 377
    |
Qy 301 TPKPATTLPPLSEATTAMGYHLKTLTLNFTISNLOQSPDMGKGSATFNSTEGVLQHLR 360
    |
Db 378 TPKPATTLPPLSEATTAMGYHLKTLTLNFTISNLOQSPDMGKGSATFNSTEGVLQHLR 437
    |
Qy 361 PLFKSSMGPFYLGCOLISLRPEKOGAATGVDTTCTYHPDPVPGGLDIOOLYWELSQLTH 420
    |
Db 438 PLFKSSMGPFYLGCOLISLRPEKOGAATGVDTTCTYHPDPVPGGLDIOOLYWELSQLTH 497
    |
Qy 421 GVTQLGFYVLDROSLFING 439
    |
Db 498 GVTQLGFYVLDROSLFING 516

RESULT 12
US-10-860-790-389
; Sequence 389, Application US/10860790
; Publication No. US20050031634A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C11
; CURRENT APPLICATION NUMBER: US/10/860,790
; CURRENT FILING DATE: 2004-06-02
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 389
; LENGTH: 833
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-860-790-389

Query Match      100.0%; Score 2321; DB 5; Length 833;
Best Local Similarity 100.0%; Pred. No. 2.4e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 60
    |
Db 78 FTHRSSVSTTSGTPTVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENWMPG 137
    |
Qy 61 SRKFTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKOGAATGDAICTHRPDPGTP 120
    |
Db 138 SRKFTTERTVLOGLLRPLFKNTSVGPLYSGCRLTLRLPEKOGAATGDAICTHRPDPGTP 197
    |
Qy 121 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 180
    |
Db 198 GLDREQLYLELSQTHSITELGPTLDRDSLYVNGFTHRSSVPTTSTGVVSEEPFTLNFT 257
    |
Qy 181 INNLRYADMADQPGSLKFNITDNVWKHLSPFLFORSSLGARYTCRVIALRSVKNGAETR 240
    |
Db 258 INNLRYADMADQPGSLKFNITDNVWKHLSPFLFORSSLGARYTCRVIALRSVKNGAETR 317
    |
Qy 241 VDLCTYLOPLSGPGLPIKQVFEHLSQOHTGILTRGYPYSLDKDSLYLNGYNEPGDEPPT 300
    |
Db 318 VDLCTYLOPLSGPGLPIKQVFEHLSQOHTGILTRGYPYSLDKDSLYLNGYNEPGDEPPT 377
    |
Qy 301 TPKPATTLPPLSEATTAMGYHLKTLTLNFTISNLOQSPDMGKGSATFNSTEGVLQHLR 360
    |
Db 378 TPKPATTLPPLSEATTAMGYHLKTLTLNFTISNLOQSPDMGKGSATFNSTEGVLQHLR 437
    |
Qy 361 PLFKSSMGPFYLGCOLISLRPEKOGAATGVDTTCTYHPDPVPGGLDIOOLYWELSQLTH 420
    |
Db 438 PLFKSSMGPFYLGCOLISLRPEKOGAATGVDTTCTYHPDPVPGGLDIOOLYWELSQLTH 497
    |
Qy 421 GVTQLGFYVLDROSLFING 439
    |
Db 498 GVTQLGFYVLDROSLFING 516

RESULT 13
US-09-778-320-206
; Sequence 206, Application US/09778320
; Patent No. US20010034052A1
; GENERAL INFORMATION:
; APPLICANT: Dillion, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, TongTong
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C5
; CURRENT APPLICATION NUMBER: US/09/778,320
; CURRENT FILING DATE: 2001-02-06
; NUMBER OF SEQ ID NOS: 301
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-320-206

Query Match      100.0%; Score 2321; DB 3; Length 914;
Best Local Similarity 100.0%; Pred. No. 2.7e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTPTGTPFVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 159 FTHRSSVSTTPTGTPFVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218

Qy 61 SKKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRDPDTPG 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 219 SKKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRDPDTPG 278

Qy 121 GLDREQLYLELSQTHSITELGPTYLDKDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 279 GLDREQLYLELSQTHSITELGPTYLDKDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 338

Qy 181 INNLRYMADMGQPSGLKFNITDNVVKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 240
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 339 INNLRYMADMGQPSGLKFNITDNVVKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 398

Qy 241 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPLYSLDKDSLYNGYNEPGDEPPT 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 399 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPLYSLDKDSLYNGYNEPGDEPPT 458

Qy 301 TKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMKGKGSANTNSTEGVLQHLR 360
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 459 TKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMKGKGSANTNSTEGVLQHLR 518

Qy 361 PLFKQSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIQQLYWELSQLTH 420
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 519 PLFKQSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIQQLYWELSQLTH 578

Qy 421 GVTQLGFYVLDKDSLSIFNG 439
    ||||||||||||||||||
Db 579 GVTQLGFYVLDKDSLSIFNG 597

RESULT 14
US-09-910-689-206
; Sequence 206, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tongtong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910,689
```

```
; CURRENT FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 206
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-689-206

Query Match      100.0%; Score 2321; DB 3; Length 914;
Best Local Similarity 100.0%; Pred. No. 2.7e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVSTTPTGTPFVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 60
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 159 FTHRSSVSTTPTGTPFVYLGASKTPASIFGPSAASHLLILFTLNFTITNLRYEENMWPG 218

Qy 61 SKKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRDPDTPG 120
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 219 SKKNTTERTVLOGLLRPLFKNTSVGPLYSGCRLLTLRPEKDGATGVDAICTHRDPDTPG 278

Qy 121 GLDREQLYLELSQTHSITELGPTYLDKDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 180
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 279 GLDREQLYLELSQTHSITELGPTYLDKDSLYVNGFTHRSSVPTTSTGVWSEEPFTLNFT 338

Qy 181 INNLRYMADMGQPSGLKFNITDNVVKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 240
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 339 INNLRYMADMGQPSGLKFNITDNVVKHLLSPLFORSSLGARYTGCVRVIALRSVKNGAETR 398

Qy 241 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPLYSLDKDSLYNGYNEPGDEPPT 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 399 VDLCTYLOPLSGPLPIKOVFHELSSQTHGITRLGPLYSLDKDSLYNGYNEPGDEPPT 458

Qy 301 TKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMKGKGSANTNSTEGVLQHLR 360
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 459 TKPATTFPLPPLSEATTAMGYHLKTLTLNFTISNLOYSPDMKGKGSANTNSTEGVLQHLR 518

Qy 361 PLFKQSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIQQLYWELSQLTH 420
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 519 PLFKQSSMGPFYLGCOLISLRPEKDGAAATGVDTTCTTYHPDPVPGGLDIQQLYWELSQLTH 578

Qy 421 GVTQLGFYVLDKDSLSIFNG 439
    ||||||||||||||||||
Db 579 GVTQLGFYVLDKDSLSIFNG 597

RESULT 15
US-09-884-441-312
; Sequence 312, Application US/09884441
; Patent No. US20020119158A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Carter, Barrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; CURRENT FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 312
```

SCORE Search Results Details for Application 10687035 and Search Result 20070607... Page 17 of 17

```
; LENGTH: 914
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-884-441-312

Query Match      100.0%; Score 2321; DB 3; Length 914;
Best Local Similarity 100.0%; Pred. No. 2.7e-200;
Matches 439; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTHRSSVTSSTGCTTIVLGASKTPASIFGSPSAASHLLILFTLNFTITNLRAYENWMPG 60
Db 159 FTHRSSVTSSTGCTTIVLGASKTPASIFGSPSAASHLLILFTLNFTITNLRAYENWMPG 218

Qy 61 SRKFNTERVILQGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 120
Db 219 SRKFNTERVILQGLLRPLFKNTSVGPLYSGCRLTLRLPEKDEATGVDAICTHRPDPTGP 278

Qy 121 GLDREQLYLELSQLTSHITELGPLYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPETLNFT 180
Db 279 GLDREQLYLELSQLTSHITELGPLYTLDRDSLTVNGFTHRSSVPTTSTGVVSEEPETLNFT 338

Qy 181 INNLRYMADMGQPSLKFNITDNVMKHLSPFORSSLGARYTCRVIALRSVKNGAETR 240
Db 339 INNLRYMADMGQPSLKFNITDNVMKHLSPFORSSLGARYTCRVIALRSVKNGAETR 398

Qy 241 VDLICTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPISLDKDSLYLNGYNEPGDEPPT 300
Db 399 VDLICTYLOPLSGPLPIKQVFHELSSQOOTHGITRLGPISLDKDSLYLNGYNEPGDEPPT 458

Qy 301 TPKPATTELPPELSEATTAMGYHLKTLTNFTLSNLQYSPDMGKGSATFNSTGVQLQHLR 360
Db 459 TPKPATTELPPELSEATTAMGYHLKTLTNFTLSNLQYSPDMGKGSATFNSTGVQLQHLR 518

Qy 361 PLFKSSKGPFFYLGCOLISLRPEKDGAAATGVDVTTCTYHPDPVPGGLDIQQLYWELSQLT 420
Db 519 PLFKSSKGPFFYLGCOLISLRPEKDGAAATGVDVTTCTYHPDPVPGGLDIQQLYWELSQLT 578

Qy 421 GVTQLGFVLDRLDSLEFNG 439
Db 579 GVTQLGFVLDRLDSLEFNG 597

Search completed: June 7, 2007, 18:04:12
Job time : 190 secs
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SCORE 2.0 BuildDate: 12/05/2005

[Score Home Page](#) [Retrieve Application List](#) [SCORE System Overview](#) [SCORE FAQ](#) [Comments / Sugg](#)

This page gives you Search Results detail for the Application 10687035 and Search Result 2007060

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: June 7, 2007, 17:49:56 ; Search time 41 Seconds
(without alignments)
1030.223 Million cell updates/sec

Title: US-10-687-035-1_COPY_14_452

Perfect score: 2321

Sequence: 1 FTHRSSVSTTSTPGTPTVYL.....HGVTLGFVLDRLDSLFING 439

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_80:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114.5	4.9	1475	2 S42718	nuclear pore compl
2	105	4.5	630	1 A46149	transcription fact
3	104	4.5	628	1 A39262	transcription fact
4	103.5	4.5	555	2 T00778	probable tRNA aden
5	102.5	4.4	2477	2 S14428	fibronectin precur
6	102	4.4	628	1 A33333	transcription fact
7	101	4.4	1426	2 T30817	homeotic protein C

8	100.5	4.3	1199	2 A40670	nuclear envelope p
9	99.5	4.3	825	2 T29634	hypothetical prote
10	99.5	4.3	1256	1 A43829	muramidase-release
11	99.5	4.3	1443	2 T02491	probable ABC trans
12	99.5	4.3	1777	2 T34369	hypothetical prote
13	99	4.3	650	2 S22835	alpha-agglutinin -
14	99	4.3	693	2 H86214	protein T6022.6 [i
15	99	4.3	837	2 H72802	minor tail subunit
16	98.5	4.2	967	2 S66852	hypothetical prote
17	98.5	4.2	1020	2 A29355	fibronectin - chic
18	98.5	4.2	1302	2 T23236	hypothetical prote
19	98	4.2	1042	2 S41705	EVI1 protein - hum
20	97	4.2	1051	2 A60191	oncogene Evi-1 - h
21	97	4.2	4936	2 AH2515	hypothetical prote
22	96.5	4.2	2664	2 T28626	variant-specific s
23	96.5	4.2	3078	2 T28432	variant-specific s
24	96	4.1	1260	2 S60896	agglutinin-like pr
25	96	4.1	1747	2 A45974	collagen alpha 1(X
26	96	4.1	1857	2 S31212	collagen alpha 1(X
27	96	4.1	1888	2 S78476	collagen alpha 1(X
28	96	4.1	3570	2 T45025	mucin MUC5B, trach
29	95.5	4.1	559	2 T40764	serine-threonine p
30	95.5	4.1	2121	2 A59233	myosin VII-like pr
31	95.5	4.1	2288	2 T30568	acetyl-CoA carboxy
32	95	4.1	875	2 AF0472	probable outer mem
33	95	4.1	1156	2 T23308	hypothetical prote
34	95	4.1	2508	2 S61441	surface-associated
35	94.5	4.1	995	2 S50358	hypothetical prote
36	94.5	4.1	1355	2 T00075	hypothetical prote
37	94.5	4.1	1787	2 G81684	kinase-related pro
38	94.5	4.1	2338	2 I73957	fiber protein - ca
39	94	4.0	543	1 ERADGG	cyclomaltodextrin
40	94	4.0	718	1 ALBSGC	cell surface glyco
41	94	4.0	1408	2 H69068	rudimentary protei
42	94	4.0	2236	1 QZFF	fibronectin precur
43	94	4.0	2386	1 FNHU	surface protein T6
44	93.5	4.0	537	2 A35400	peptide synthetase
45	93.5	4.0	3603	1 D69681	

ALIGNMENTS

RESULT 1

S42718

nuclear pore complex protein nup153 - human

C:Species: Homo sapiens (man)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004

C:Accession: S42718; S37477

R:McNorrow, I.; Bastos, R.; Horton, H.; Burke, B.

Biochim. Biophys. Acta 1217, 219-223, 1994

A:Title: Sequence analysis of a cDNA encoding a human nuclear pore complex protein, hn

A:Reference number: S42718; MUID:94154002; PMID:8110839

A:Accession: S42718

A:Molecule type: mRNA

A:Residues: 1-1475 <NCM>

A:Cross-references: UNIPROT:P49790; UNIPARC:UPI000012FC15; EMBL:Z25535; MID:9406224; P

Query Match 4.9% Score 114.5; DB 2; Length 1475;

Best Local Similarity 19.3%; Pred. No. 2.8; Indels 133; Gaps 16;

Matches 80; Conservative 53; Mismatches 149;


```
QY 17 TVYLGASKTPASIFGSAASHLLILFLTNFTITNLR-----YEENMMGSRKRENTTE 68
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 380 SVYFKPSLTPSG-----EFRKTNQRIIDNKCSTGYEKNMTPGQNR-----E 419

QY 69 RVQGLLRPLPKNTSVGPLYSGCRLTLRLRPEKDEATGVDAICTHRPDPGTGGLDRQQLY 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 420 QRESGFSYPNFS-----LPAANGLSGSGVG-----GGCKRRRERH 454

QY 129 LEISQLTHSITELGPYTLDRSLVNGFTHRSSVPT---TSTGVVSEEPFTLNFT---INN 183
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 455 AFVASKPLREEEMEVEVLPKLSLPTS-----SSLPFTNFSSPEITTSPPSPINSQALTN 510

QY 184 LRYMDMGQPGSLKFNITDNVMKHLSPILFORSSILGARYTCGRVIALRSVKNGAETRVDL 243
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 511 KVQMTSPSSGSPMFKFSSPIVKSTEANVLPSSIG--FTFSVPVAKTAELSGSSST--- 565

QY 244 LCTYLOPLSGPLPIKQVPHLSQOOTHGITRL-----GPY---SLDKOSLY 286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 566 ----LEPI-----ISSAHVTVTNSTNCKKTPPEDCEGFPFPAEILKEGSV 608

QY 287 LNGYNEPGDEP-----PTTPKPATTELPPLSEATTAMGYHLKTLTLNFTISNLQYS 338
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 609 LDILKSPGFASPKIDVAAQATPATSVPVYTRPAIS-----SFSGSLGFG 653

QY 339 PMKGKSATFNSTEGVLQHLRLPIQKSSMGPFYLGQCLISIRPEKDKGAATGVD 393
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 654 ESLKAGSSWQCDT-----CLIQNKVTDNKCIAQAAKLSPRDTAKQTGIET 699
```

```
RESULT 2
A46149
Transcription factor HNF-1A - hamster
N:Alternate names: hepatic nuclear factor 1-alpha; transcription factor Lf-B1
C:Species: Cricetinae gen. sp. (hamster)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A46149
R:Emens, L.A.; Landers, D.W.; Moss, L.G.
Proc. Natl. Acad. Sci. U.S.A. 89, 7300-7304, 1992
A:Title: Hepatocyte nuclear factor 1 alpha is expressed in a hamster insulinoma line a
A:Reference number: A46149; MUID:92366449; PMID:1380153
A:Accession: A46149
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-630 <EME>
A:Cross-references: UNIPROT:Q7M0C7; UNIPARC:UPI0000173313
A:Experimental source: HIT-T15 M.2-2-2 insulinoma cell line
A:Note: sequence extracted from NCBI backbone (NCBIP:110643)
C:Complex: homodimer; can also form heterodimers with, for example, HNF-1B
C:Function:
A:Description: transcription activator required for the expression of a number of live
A:Note: also expressed in some other tissues, where it may play other roles
C:Superfamily: transcription factor HNF-1; homeobox homology
C:Keywords: DNA binding; homeobox; liver; nucleus; transcription regulation
F:1-33/Region: dimerization
F:222-277/Domain: homeobox homology <Hox>
```

```
Query Match 4.5% Score 105; DB 1; Length 630;
Best Local Similarity 21.4% Pred. No. 4.2;
Matches 89; Conservative 55; Mismatches 137; Indels 134; Gaps 20;
```

```
QY 5 SSVSTSTSTGTFTVYLGASKTPASIFG-----PSAASHLLILFLTNFTITNLRVE 54
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 297 ATLSAHSSPGLPTSALSPKSVGVRYGQPATSEAAEVSPSSGGPLV-----TVAAPLHQ 350

QY 55 ---ENKMPGSRKFKTTERVLOGLLRPLPKNTSVGPLYSGCRLTLRLRPEKDEATGVDAIC 111
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 351 VSPGTGLEPSSSLSTEAKLV-----SATGGPLPVPVSTLTAL----- 386

QY 112 THRDPDTGGLDREQLYLELSQTHSIT-----ELGP-YTLDRDSLYVNGF---THRSS 161
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 387 -HNLEQTSGLNQOPQNLINASLPQVMTIGFGEPAISLGTFTNTGTASTLVIGLASQAQS 445

QY 162 VP-----TTSTGVVSEEPFTLNFT-----INNLRVMDMGQPGSLKFNITD 202
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 446 VPVINSMGSSLTTLQPVQFSQPLHPSYQQPLMPVQSHVQAQSPFWATMAQ----- 495

QY 203 NVMKHLISP--LFORSSILGARYTCGRVIALRSVKNGAETRVDLCTYLOPLSGPLPIKQ 260
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 496 ----LQSPHALYSKPEVAQYTHTSLLPQTMLI--TDTNLSALASL-----TFTKQ 540

QY 261 VFHELQOOTHGITRLGYPYSLDKDSLNGYNEPGDEPPTTPKPATTELPPLSEATTAMG 320
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 541 VFTSDTEAS-----SEGLHEPSS---PATTHIPSQDPSIQ-- 575

QY 321 YHLK---TLTNFTISN----LQYSPDMGKG-SATENSTEGVLQHLRLPLFKSS 367
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 576 -HLQPAHRLSTSPVSSSLVLYQSSDSTNGSHLLPSNHGVIERFISTQMASSS 629
```

```
RESULT 3
A39262
Transcription factor HNF-1A - mouse
N:Alternate names: hepatic nuclear factor 1-alpha; transcription factor APf; transcrip
C:Species: Mus musculus (house mouse)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A39262; S70436
R:Kuo, C.J.; Conley, P.B.; Hsieh, C.L.; Francke, U.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 87, 9838-9842, 1990
A:Title: Molecular cloning, functional expression, and chromosomal localization of mou
A:Reference number: A39262; MUID:91088607; PMID:2263635
A:Accession: A39262
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-628 <KUO>
A:Cross-references: UNIPROT:P22361; UNIPARC:UPI0000029283; GB:M57966; NID:g193885; PID
R:Bach, I.; Pontoglio, M.; Yaniv, M.
Nucleic Acids Res. 20, 4199-4204, 1992
A:Title: Structure of the gene encoding hepatocyte nuclear factor 1 (HNF1).
A:Reference number: S70435; MUID:92375726; PMID:1354855
A:Accession: S70436
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 199-279 <BAC>
A:Cross-references: UNIPARC:UPI0000173312
A:Note: only a part of the nucleic acid sequence is shown
C:Genetics:
A:Gene: Hnf-1
A:Introns: 238/2
A:Note: the list of introns is incomplete
C:Complex: homodimer; can also form heterodimers with, for example, HNF-1B
C:Function:
```